

## Search Report

## STIC Database Tracking Number: 228790

To: PATRICIA DUFFY

Location: REM-3B05 / Mailbox 3C18

**Art Unit: 1645** 

Thursday, June 28, 2007

Case Serial Number: 09/955502

From: HUGH YOUNG Location: EIC 1600 REM-1D58 / REM-1A64

Phone: (571)272-5722

hugh.young2@uspto.gov

## **Search Notes**

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Hugh P. Young Ph.D. ASRC Management Services USPTO Contractor/EIC1600



STIC-BIOLECH/CHEITILID	0 1001		1 10.
From: Sent: To: Subject:	Duffy, Patricia Friday, June 22, 2007 6:24 PM STIC-Biotech/ChemLib sequence search		
Importance:	High	i.	ET (ED)
	D:11. II — QQ — 9/ ial and interference database search. 5 hits and deliver to examiner.		
Patricia A. Duffy, Ph.D. Primary Patent Examiner 571-272-0855, Remsen 3B05, Mailbox: 3C18			
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Mg			
***********  Searcher Phone: Date Searcher Picked up: Date completed: Searcher Prep Time: Online Time:	************  Type of Search  NA# AA#:  S/L: Oligomer:  Encode/Transl:  Structure #: Text:  Inventor: Litigation:	,	*************************  /endors and cost where applicable STN:     DIALOG:     QUESTEL/ORBIT:     LEXIS/NEXIS:     SEQUENCE SYSTEM:     WWW/Internet:     Other (Specify):

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

June 27, 2007, 11:05:06; Search time 39 Seconds (without alignments) 224.506 Million cell updates/sec

US-09-955-502A-11 486 1 MSRTIFCTFLQREAEGQDFQ.....NFLFEGKEVHIEGYTPEDKK 91 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 3 6 4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hymothetical prote	100		conserved hypothet	conserved hypothet	conserved hypothet	hypothetical prote	hypothetical prote			conserved hypothet	fumarate hydratase	fumarate hydratase	63K antigen - nema	protein unc-73b [i	guanine nucleotide	hypothetical prote	hypothetical prote		probable fumarase	ABC transporter at	hypothetical prote	10	60K filarial antig	_	translation activa		_	hypothetical prote	
SUMMARIES	ū	A85954	265082	F91108	AH0879	C82320	A10116	C64013	E84994	H83003	C82624	H81014	C81063	A81807	A54510	D87749	T42739	AC2256	T46013	T16527	A83105	A99574	A97991	B95121	A28209	T15842	A48126	164172	G65212	T05429	
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A7046 JC207 C6409 C6409 F8390	T14594 WMTMPV WMTMPV STSET E84106 C96667 B71071 T04325 T00661
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## ALIGNMENTS

hypothetical protein yggX [imported] - Bscherichia coli (strain O157:H7, substrain EDL933 C;Species: Bscherichia coli

Cipate: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004
CjAccession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: A85954

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-91 <STO> A;Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:g12517511; Pl A;Experimental source: strain O157:H7, substrain EDL933

Genetics:

A;Gene: yggX C;Superfamily: fe(II) trafficking protein YggX

100.0%; Score 486; DB 2; Length 91;

Query Match

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R. Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Vibrio cholerae (strain N16961 serogro
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A,Experimental source: serogroup Ol; strain N16961; biotype El Tor
                                                                                                                                                              conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica C,Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C,Pate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP1000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
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R; Heidelberg, J. F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Mature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833; PMID:10952301
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C,Species: Vibrio cholerae
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
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ilarity 94.5%; Pred. No. 7.9e-40;
Conservative 5; Mismatches 0
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                                  HHKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
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C,Superfamily: fe(II) trafficking protein YggX
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C;Superfamily: fe(II) trafficking protein YggX
             EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
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es 86; Conserv
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Matches 75; Conserv
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A;Molecule type: DNA
A;Residues: 1-90 <HEI>
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A;Residues: 1-91 <PAR>
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Matches 86
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A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX
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K; Abayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Cross-references: UNIPROT:P52065; UNIPARC:UP1000163A04; GB:BA000007; PIDN:BAB37261.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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100.0%; Score 486; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0;
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         Pred. No. 1.6e-41;
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C;Superfamily: fe(II) trafficking protein YggX
                                91; Conservative
         Best Local Similarity
Matches 91; Conserva
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A;Molecule type: DNA
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Conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01) C; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Species: Is-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004 C; Accession: H83003 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004 C; Accession: H83003 #s. Dram, X.Q.; Erwin, A.L.; Mizoquchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 #squence of Pseudomonas aeruginosa PA01, an opportunistic pathox A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathox A; Reference number: A82950; MUID:20437337; PMID:10984043
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A, Molecule type: DNA
A, Residues: 1-90 <STO>
A, Cross-references: UNIPARC: UPI00000C5F26; GB: AE004927; GB: AE004091; NID: g9951437; PIDN: A, Experimental source: strain PAO1
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               C;Species: Buchnera sp.
C;Accession: B84994
R;Shigenobu, S; Watanabe, H; Hattori, M; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S; Watanabe, H; Hattori, M; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Reference punder: B8499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-93 sSTO>
A;Residues: 1-93 sSTO>
A;Coss-references: UNIPARC:UPI000005E610; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
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hypothetical protein [imported] - Buchnera sp. (strain APS)
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Best Local Similarity 61.8%; Pred. No. 1.6e-19;
Matches 47; Conservative 16; Mismatches 13
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47.5%; Score 231; DB 2;
Best Local Similarity 51.7%; Pred. No. 3.7e-16;
Matches 45; Conservative 10; Mismatches 32;
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C, Superfamily: fe(II) trafficking protein YggX
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77 EHRKKIEKYMKLFLFK 92
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C82624
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C;Superfamily: fe(II) trafficking protein YggX
                                                                                                                                                                                                                                                                                                R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022; C;Genetics:
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                     - Yersinia pestis (strain CO92)
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
                                                                                                                                                                                                           C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
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82.2%; Pred. No. 1.4e-32;
live 8; Mismatches 8;
                                                                                                                                                                                  conserved hypothetical protein YP00953 [imported]
EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
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Best Local Similarity 82.2.
Best Total Similarity
T4; Conservative
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nes 68; Conser
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Molecule type: DNA
Residues: 1-90 <KUR>
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C;Accession: A10116
R;Parkhill, J.; Wren
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C;Superfamily: 1
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A;Status: preliminary A;Molecule type: DNA

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fumarate hydratase, class I NWB1613 [imported] - Neisseria meningitidis (strain MC58 serr
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.E.; Eisen, J.A
Dougherty, B.A.;
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A,Experimental source: serogroup B, strain MC58
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A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
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A,Experimental source: serogroup A, strain 22491
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C;Keywords: carbon-oxygen lyase; hydro-lyase
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
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                                                                                                                                                    Gaps
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                                                                                                                                                33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                              Length
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311 YSPDNGKRVDVDKLIKEEVASWKTGDVLLLNGKILTGRDAAHKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                      43.8%; Score 213; DB 2;
44.3%; Pred. No. 2.2e-14;
tive 16; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Mismatches
C;Superfamily: fe(II) trafficking protein YggX
                                                                                                                                                                                                                                                                                                                                                                                  61 EHRKLLEQEMVNFLFEGKEVHIEGYTPE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.0%; Score 78; 30.2%; Pred. No.
                                                      Query Match
Best Local Similarity 44.3%;
Marches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-507 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-546 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVD 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A81807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: NMB1613
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                                                                                                                                                                                                                                                                                                                                Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P. Briones, M.S.; Bueno, M.R.P.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. as-locena, C.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. abriones, Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. Bueno, W.C.A.; Frey, J. S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.; Marrino, C.L.; Marques, M.V.; Martins, B.M.F.; Mathors: Martins, B.M.F.; Mathors, M.C.; Frohm J. W.C., M.; Marca, B.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.M.; Silva, Jr., Wah, ida Silvai, M.Y.; Mathors, da Silva, A.C.R.; da Silva, F.R.; Salveilli, R.V.; Sawasak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
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A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence revision 31-Mar-2000 #נאזר האאחתם הכ-החד-2004
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A;Molecule type: DNA
A;Residues: 1-88 cTET>
A;Cross-treferences: UNIPARC:UPIO0000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A;Cross-treferences: UNIPARC:UPIO0000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
*Residues: 1-88 ×PAR>.
A;Cross-references: UNIPARC:UPIO0000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                 A;Residues: 1-105 <SIM>
A;Cross-references: UNIPARC:UP100000C288F; GB:AE004010; GB:AE003849; NID:g9106992; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: H81014; F81958 -- - 'Accession: H81014; F81958 -- 'Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; ickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. i, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. cience 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;IILLE: COMPLETE DNA SEQUENCE Of a SEROGROUP A STRAIN Of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: F81958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNA
                                   A;Title: The genome seguence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 226; DB Z; 50.6%; Pred. No. 1.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SHRAFLEEELNKFLFERRVAKPEGYIEPD 104

RESULT 11 H81014

A; Gene: NMB2021; NMA0419

A;Status: preliminary

A; Accession: H81014

EHRKLLEQEMVNFLFEGKEVHIEGYTPED

16 61

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A,Gene: XF1908 C,Superfamily: fe(II) trafficking protein YggX

M.; Tsuhako, M.H.; Vallada. A;Reference number: A59328

A;Contents: C;Genetics: 10;

Conservative

Best Local Similarity Matches 45; Conserv

Query Match

89

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C;Species: Caenorhabditis elegans
C;Dacte: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42739; T42740; T34427; T34430; T34426
R;Steven, R.; Kubiseski, T.J.; Zheng, H.; Kulkarni, S.; Mancillas, J.; Ruiz Morales, A.;
Cell 92, 788-795, 1998
A;Title: UNC-73 activates the Rac GTPase and is required for cell and growth cone migrat: A;Reference number: Z22256; MUID:98188103; PMID:9529254
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A;File: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-1634,'ON',1637,'E' <ST2>
Cross-references: UNIPARC:UP1000002A21C; EMBL:AF048835; NID:g2944397; PIDN:AAC12932.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 7/3; 64/2; 95/3; 230/3; 265/2; 335/3; 360/3; 488/3; 569/1; 695/1; 1028/2; 106
19/3; 2262/2; 2331/1; 2351/3; 2396/1; 2431/1
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: mRNA
A;Residues: 1-2488 cSTE>
A;Cross-references: UNIPROT:061528; UNIPARC:UPI00000611F8; EMBL:AF048834; NID:g2944395;
A;Accession: T42740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,Molecule type: DNA
Skedidues 1-2488 sOUZ>
;Cross-references: UNIPARC:UPI0000611F8; EMBL:U80436; PIDN:AAC71108.1; GSPDB:GN00019;
;Experimental source: strain Bristol N2; clone F55C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA Residues: 1-1634,'0N',1637,'E' <DU2>
Residues: 1-1634,'0N',1637,'E' <DU2>
Cross-references: UNIPARC:UPI000002A21C; EMBL:UB0436; PIDN:AAC71109.1; GSPDB:GN00019; Experimental source: strain Bristol N2; clone F55C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 'MTKCFT',1568,'LRK',1572-2488 <DU3>
A;Cross-references: UNIPARC:UP100002A21D; EMBL:U80436; PIDN:AAC71110.1; GSFDB:GN0019;
A;Experimental source: strain Bristol N2; clone F55C7
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2256
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ص
                                                                                                                                                          guanine nucleotide exchange factor unc-73a - Caenorhabditis elegans
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1168 GENGS---TQSSKDEFSLDRHSDTAIFNEKKINERREENRKWLE 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: unc-73; F55C7.7a; unc-73; F55C7.7b; CESP:F55C7.7c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribu, Z.; Le, T. submitted to the EMBL Data Library, November 1996 submitted to the EMBL Data Library, November 1996 A;Description: The sequence of C. elegans cosmid F55C7. A;Reference number: Z21524 A;Reference number: Z21524 A;Accession: T34427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
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Best Local S:
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog; Reference number: A75000, MUID:99069613; PMID:9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: see websites genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-548 <PER>
A;Cross-references: UNIPROT:P10723; UNIPARC:UPI00001365DB; GB:J03971; NID:g156056; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Brugia malayi
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Datession: A54510
E;Accession: A54510
Mol. Biochem. Parasitol. 30, 97-104, 1988
A;Title: A multi-copy gene encodes a potentially protective antigen in Brugia malayi. A;Accession: A54510; MUID:88288341; PMID:2840577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                      7
                                                                                                                                                                 A;Introns: 23/2; 79/3; 140/1; 163/3; 214/1; 276/3; 321/3; 379/3; 433/3; 481/3
C;Superfamily: lysine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQ-WQH-KQTMLINEKKLNMMNA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D87749 Elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 RTLYQAMIITKSSKGDFLIRTKKDGKQIWEAASKTALKKSWRHYEQEMLKNEKVA----
                                                                                                                                 22 YPGELGKRI-YNEISKEAWAQWQHKQTMLINEKKLINMMNAEHRKLLEQEMVNFLFEGKEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.6%; Score 76; DB 2; Length 548; Best Local Similarity 30.7%; Pred. No. 7.7; Matches 27; Conservative 16; Mismatches 31; Indels
      Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNAEHRKLLE
                                                                   20;
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Pred. No. 30;
9; Mismatches 15;
      DB 2;
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   16.0%; Score 78; DB 2 30.2%; Pred. No. 4.8; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AKMLEKDATEVGVKAALBEAKKVQIE 103
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    nematode (Brugia malayi)

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38.6%;
                                                                   Conservative
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Residues: 1-1638 <STO>
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Best Local Similarity
Matches 17; Conserv
      Query Match
Best Local Similarity
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PVD 407
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                                                                   19;
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Gaps

16;

22; Indels

Length 447;

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C;Accession: A83105
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A.Reference number: A82950; MUID:20437337; PMID:10984043
A.Accession: A83105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase al
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Nucleic Acids Res. 29, 2145-2153, 2001
A;fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A99574
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A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP10000C5CC5; GB:AE004849; GB:AE004091; NID:g9950550; PIDN:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                              13 EAEGODFOLYP----GELGKRI-YNEISKEAWAQWQHKQTWLINEKKLNMMNAEHRKL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                             23 PGELGKRIYNEISKEAWAQWQHKQTWLI--NEKKLNWM-NAEHRKLLEQEMVNFLFEGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable fumarase PA4333 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                            Query Match
14.8%; Score 72; DB;
Best Local Similarity 32.9%; Pred. No. 15;
Matches 24; Conservative 11; Mismatches
A; Introns: 125/3; 191/3; 228/2; 322/2; 404/3
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354 IGIQNNKNFTDED 366
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                             80 VHIE---GYTPED 89
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A Molecule type: DNA
A;Residues: 1-507 <STO>
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Matches 22; Conserv
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                           A;Molecule type: DNA
A;Residues: 1-683 «KUR»
A;Cross-references: UNIPROT:Q8YR48; UNIPARC:UPI0000CE850; GB:BA000019; PIDN:BAB75301.1;
A;Experimental source: strain PCC 7120
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K;Heunes, V.; Wurmbach, B.; Dizonak, II.; Ancorgo, W.; Mewes, H.W.; Lemcke, K.; Mayer, K. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223019
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;Experimental source: strain Bristol N2
                                                                                                                             A, Experimental Boulder Boulder Brown Street Brown Synechocystis long-chain-fatty-acid-CoA ligase, acetate-CoA ligase C, Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase, acetate-CoA ligase C, Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase, acetate-CoA ligase C, Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase, acetate-CoA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| : : | : | : | : | : | 568 GQDQR----SIGALIVPNV--EALAKWAESQNLVLSVEDDNLTSSSSQKINLESKMIQGL 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLI--NEKKLNMMNAEHRKL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T10K17.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Caenorhabditis elegans
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T16527
                                                                                                                                                                                                                                                                                                                                                                                                                               GODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAEHRKL-LEQEMVNFL
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                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%; Score 72; DB 2; Length 265; llarity 31.2%; Pred. No. 8.4; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                        Query Match 15.3%; Score 74.5; DB 2; Length 68: Best Local Similarity 28.4%; Pred. No. 14; Matches 23; Conservative 21; Mismatches 24; Indels
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A;Molecule type: DNA
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622 FR-QELINREVONRPGYRPDDR 641
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A;Introns: 42/3; 224/3; 246/3
A;Note: T10K17.120
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                               16
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12;

Length 507; 28; Indels 5

Gaps

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Indels

28;

Length 511;

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C,Accession: A28209
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Perrine, K.G.; Denker, J.A.; Nanduri, J.; P.A.; Natisen, T.W.; Maroney, P.A.; Goodwin, R.G.; Perrine, K.G.; Denker, J.A.; Nanduri, J.; P.A.; Title: Cloning and characterization of a portentially protective antigen in lymphatic final A; Reference number: A28209; MUD:88217950; PMID:3368467
A,Mocession: A28209
A,Mocession: A28209
A,Mocession: A28209
A,Mocession: A28209
A,Residues: 1-548 «NIL»
                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:P10723; UNIPARC:UP1000016B881; EMBL:J03266; NID:g156052; PIDN
C,Superfamily: lysine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q18859; UNIPARC:UP10000179EB3; EMBL:U40410; NID:g1065453; PII
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:C54G7.4
A;Introns: 6/3; 70/1; 111/2; 160/3; 180/1; 277/1; 325/3; 367/3; 395/3; 430/3; 494/1; 512,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 CTFTRLAVIKLVEQVPFQFLLYEFDGDELKLÍÝTSDKRDVWDYEWDQNNSNMLALKDKQK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CTFLQ----REAEGODFQL----YPGELGKRIYNEISKEAW-AQW-QHKQTMLINEKKLN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C54G7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                          C;Species: Brugia_malayi
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQ-W-QHKQTMLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tex
C;Accession: T15842
R;Du, S
R;Du, S
B;Du, S
B;Du, S
B;Du;Di, S
B;Du;Di, S
B;Description: The sequence of C. elegans cosmid C54G7.
A;Reference number: Z18416
A;Accession: T15842
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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; Pred. No. 86;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.2%; Score 69; DB 28.4%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
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28.7%;

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80 VHIE 83
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-258 «KUR>
A;Cross-references: UNIPROT:Q97QZO; UNIPROT:Q8CYT2; UNIPARC:UPI000004A8FC; GB:AE005672;
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: Q97QZ0; UNIPROT: Q8CYT2; UNIPARC: UPI000004A8FC; GB: AE007317;
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
                                                                                                                                                                                                                                                                                       C; Species: Streptococcus pneumoniae
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Accession: A97991
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; y, P.; Sun, P.M.; Winkler, M.E.
A; Bacteriol, 183, 5709-5717, 2001
A; Authors ang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID: 21429245; PMID: 11544234
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  QDFQLYPG-ELGKRIYNEISKEAWAQWQHKQTMLINEKKLLNMMNAEHRKLLEQEMVNFLF
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                                                                                                                                            142 EKREI-IQSLNKKQQK 156
                                                                                               EGKEVHIEGYTPEDKK 91
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Residues: 1-258 <KUR>
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IKVD 72
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Superoxide damage, cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
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1 MSRTIFCTFLQREAEGQDFQ.....NFLFEGKEVHIEGYTPEDKK
GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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Maximum Match 100%
Listing first 75 summaries
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	57	ö	₩.	285	4,	AAB92683		Aab92683	Human	
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the mative amount of vggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. VggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from of (He-S) clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                 Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
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ABB78161 standard; protein; 91 AA (first entry) 05-NOV-2002 ABB78161; 

Amino acid sequence of a YggX homologue.

Superoxide damage, cell, YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.

Unidentified

US2002072118-A1.

13-JUN-2002

18-SEP-2001; 2001US-00955502

22-SEP-2000; 2000US-0234588P

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DOWNS D. GRALNICK J A.

WPI; 2002-589476/63.

Gralnick JA;

Downs D,

Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.

Example; Fig 1A; 16pp; English

The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues

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hydroxyl radical; DNA damage; YggX homologue.
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Score 469; DB 5; 1
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86; Conservative
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cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterior serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Pe-S) clusters, and thus reduces the loss of Pe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer
                                      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSRTIFCTYLQRDAEGODFOLYPGELGKRIYNEISKDAWAQWQHKQTWLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radicals and thus reduced DNA damage. The method is useful superoxide damage in a bacterial, yeast, mammalian or plant 378147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for reducing superoxide damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing superoxide damage to a cell, e.g. bacterial, mammalian cell, comprises engineering the cell to produce more YggX protei protein identified from Salmonella enterica Serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.6%; Score 455; DB 5; Length 91; 92.3%; Pred. No. 1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHRKLLEGEMVSFLFEGKDVHIEGYPTEDKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification describes a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB78160 standard; protein; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 1A; 16pp; English
                                                                                                                                                                                                                                     18-SEP-2001; 2001US-00955502
                                                                                                                                                                                                                                                                                  22-SEP-2000; 2000US-0234588P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Conservative
                                                                                                           Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                            Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxyl radicals and
                                                                                                                                                                                                                                                                                                                               DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-589476/63.
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Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002072118-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 91 AA;
                                                                                                                                                                                                                                                                                                                          SNWOG (/NWOG)
                                                                                                                                                                                               13-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                            Downs D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINEKKLNMMNA 60
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                                                                                                                                                                                                                                                                                  Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , e.g. bacterial, mammalian or
to produce more YggX protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing superoxide damage to a cell, e.g. bacterial, mammalian cell, comprises engineering the cell to produce more YggX protei protein identified from Salmonella enterioa Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification describes a method for reducing superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 469; DB 5; Length 91; Pred. No. 3.2e-46;
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EHRKLLEQEMVSFLFEGKDVHIEGYTPEDKK 91
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                                                                                                                                                                                                                                       Amino acid sequence of a YggX homologue
                                                                                                         ABB78162 standard; protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 1A; 16pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-2000; 2000US-0234588P.
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1 Similarity 94.5%;
86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DOWN/) DOWNS D.
(GRAL/) GRALNICK J A.
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                                                                                                                                                                                                                                                                                                                                               Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                         JS2002072118-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 91 AA;
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                                                                                                                                                    ABB78162;
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RESULT 7
ABB78163
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                                                                                                                                                                                cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for
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                                                                                                                                                                        The specification describes a method for reducing superoxide damage to
                                                                                                                                                                                                                                                                                                                                                            1 MSKTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTWLINEKKLNWWNA
                                                                                                                                                                                                                                                                                                                                                1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                       reducing superoxide damage in a bacterial, yeast, mammalian or plant
cell. ABB78147-78 represent YggX homologues
                                                                                                            Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                        Length 88;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                        Score 453; DB 5;
Pred. No. 2.2e-44;
5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae polypeptide seqid 11962.
                                                                                                                                                                                                                                                                                                                                                                                        61 EHRKLLEQEMVNFLFEGKEVHIEGYTPE 88
                                                                                                                                                                                                                                                                                                                                                                                                    HIKILLEQEMVSFLFEGKDVHIEGYTPE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO65445 standard; protein; 107 AA
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                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                     Example; Fig 1A; 16pp; English
                                                                                                                                                                                                                                                                                                        93.2%;
94.3%;
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18-SEP-2001; 2001US-00955502
                     22-SEP-2000; 2000US-0234588P
                                                                                                                                                                                                                                                                                                                              83; Conservative
                                                                      Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae.
                                      (DOWN/) DOWNS D.
(GRAL/) GRALNICK J A.
                                                                                        WPI; 2002-589476/63.
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N-PSDB; ACH98996.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      Sequence 88 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO65445;
                                                                      Downs D,
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                                                                                                                                                    The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 MSRTIFCTFLQREADGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLSMMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding an Enterobacter cloacae polypeptide, useful detecting, preventing, and treating pathological conditions resulting from bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; vaccine; bacterial infection; enterobacter infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 450; DB 7; L
Pred. No. 6.3e-44;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacter cloacae protein amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHRKILEQEMVOFLFEGKDVHIEGYTPPEKQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                                                                                                 Disclosure; SEQ ID NO 11962; 932pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEH63450 standard; protein; 126 AA
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98US-0094145P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 92.6%;
1 Similarity 91.2%;
83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107 AA;
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Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                            Amino acid sequence of a YggX homologue.
              EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                   ABB78165 standard; protein; 90
                                                                                                                                                                                                                                                                                                                .8-SEP-2001; 2001US-00955502
                                                                                                                                                                                                                                                                                                                                         22-SEP-2000; 2000US-0234588P
                                                                                                                                                   05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-589476/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 90 AA;
                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                        13-JUN-2002.
              61
                                                                                                                          ABB78165;
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                                                                                                                                                                                                                                                                                                                                                                 DOWN/)
                                                                                                                                                                                                                                                                                                                                                                             (GRAL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Pe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for
                                                                                                   9
                                                                                                                 Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a method for reducing superoxide damage to
                                                                                                   1 MSRTIPCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNNA
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reducing superoxide damage in a bacterial, yeast, mammalian or plant
                                                                          ö
                                                  Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 90;
                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                               ; DB 10;
3.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 402; DB 5;
Pred. No. 1.8e-38;
                                                                                                                                                                 HIRLIEQEMVNFLFEGKDVHIEGYTPPEK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell. ABB78147-78 represent YggX homologues
                                                  Score 436; DB
Pred. No. 3.2e
6; Mismatches
                                                                                                                                                   61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                               Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                      ABB78155 standard; protein; 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 1A; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-2001; 2001US-00955502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2000; 2000US-0234588P.
                                               ch 89.7%;
1 Similarity 88.9%;
80; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-589476/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 75; Conserv
                                                             Best Local Similarity
                         Sequence 126 AA;
                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                    US2002072118-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOWN/) DOWNS
(GRAL/) GRALNI
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 invention
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                                                  Query Match
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                                                                         Matches
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                                                                                   cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification describes a method for reducing superoxide damage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 1A; 16pp; English
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ID ABB7
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AC ABB7
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1 MSRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLINMMNA

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The invention relates to new Proteus mirabilis polypeptides andi...
polymucleotides, The invention also relates to antibodies against the
polymetides, methods for producing the polypeptides, amethod of
generating vaccines for immunishing an individual against P. mirabilis, a
method for evaluating a compound for the ability to bind a P. mirabilis
polypeptide and a method for screening test compounds for anti-bacterial
activity. The polypeptides and polymucleotides are useful as molecular
targets for diagnosing, preventing and treating pathological conditions
resulting from bacterial infection, as reagents for diagnosis of
bacterial diseases, as components of antibacterial vaccines, as targets
for antibacterial days or as bio-control agents for plants. This
sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MSRTIFCTFLNKEADGLDFQLYPGELGKRIFNEISKEAWGÓWMAKOTMLINEKKLNTMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWOHKQTMLINEKKLNNMNA
                                                                                                                                                                                                                                                                                                         New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 80.0%; Score 389; DB 7; Local Similarity 80.0%; Pred. No. 6.1e-37; tes 72; Conservative 7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superoxide damage; cell; YggX; Salmonella en
hydroxyl radical; DNA damage; YggX homologue
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5443; 870pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRKLLEOEMVRFLFEGHDVHIDGYTPPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB78150 standard; protein; 91 AA
                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                   biocontrol agents for plants.
                                                              05-APR-2000; 2000US-00543681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-2001; 2001US-00955502
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                                                                                                                                                                                                                                             WPI; 2003-895291/82.
                                                                                                                                                                                                                                                                    N-PSDB; ADF00986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                            09-APR-1999;
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                                                                                                                                                                                                      Breton GL;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the mative amount of 'ggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                       Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 395, DB 5; Length 78;
Pred. No. 1e-37;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell. ABB78147-78 represent YggX homologues
                                                                  Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF05158 standard; protein; 93 AA
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                                                                                                                                                                                                                                                                                                                                                               22-SEP-2000; 2000US-0234588P.
                                                                                                                                                                                                                                                                                                                18-SEP-2001; 2001US-00955502
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Best Local Similarity 94.9%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gralnick JA;
                                                                                                                                                                               Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                        (DOWN/) DOWNS D. (GRAL/) GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-589476/63
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                                                                                                                                                                                                                           US2002072118-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78 AA;
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Gaps

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Length 93; 11; Indels enterica serovar typhimurium;

RESULT 14

g ò ADP05158

IID ADP0

XX ADP0

XX ADP0

XX DDT

III 12-F

XX ADP0

X

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cell. The method comprises a method for reducing superoxide damage to a call. The method comprises engineering the cell to produce more than the native amount of YagX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YagX reduces the oxidation of (Re-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YagX homologues
                                                                                                                                          plant
                                                                                                                                     Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                             Example; Fig 1A; 16pp; English
                                             Gralnick JA;
(GRAL/) GRALNICK J A.
                                                                                          WPI; 2002-589476/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91 AA;
                                             Downs D,
SXCXCCCCCCXXXXFFFFXXXXCCCCCCCCCXXXX
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1 MARMVFCERLKQEAEGLDFQLYPGELGKRIFDSISKQAMGEWMKKQTMLVNEKKLNMMNA 1 MSRTIFCTFLOREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA Gaps .; 0 79.8%; Score 388; DB 5; Length 91; 76.9%; Pred. No. 7.8e-37; ive 11; Mismatches 10; Indels 91 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91 Query Match Best Local Similarity 76.94 Matches 70; Conservative 61 61 셤 Š

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ABB78152 standard; protein; 87 05-NOV-2002 ABB78152; RESULT 16 

Amino acid sequence of a YggX homologue. (first entry)

cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue. Superoxide damage;

Haemophilus influenzae.

US2002072118-A1

13-JUN-2002.

18-SEP-2001; 2001US-00955502

22-SEP-2000; 2000US-0234588P

DOWNS D. GRALNICK J A. (DOWN/) 1 (GRAL/) (

Gralnick JA;

Downs D,

WPI; 2002-589476/63.

Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.

cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues

Example; Fig 1A; 16pp; English

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cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterios servoar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                     Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
            specification describes a method for reducing superoxide damage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification describes a method for reducing superoxide damage to
                                                                                                                                                                                                                                                                     1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                            87;
                                                                                                                                                                                                        79.6%; Score 387; DB 5; Length 87
78.2%; Pred. No. 9.6e-37;
tive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                EHRKLLEQEMVNFLPEGKEVHIEGYTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002 (first entry)
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-589476/63
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002072118-A1.
                                                                                                                                                                            Sequence 87 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB78151;
                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ( /NIMOQ )
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                         Amino acid sequence of a YggX homologue.
                EHRKLLEQEMVNFLFEGKEVHIEGYTP
                                                                                                     ABB78154 standard; protein; 88
                                                                                                                                                                                                                                                                                                                                                      18-SEP-2001; 2001US-00955502.
                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-2000; 2000US-0234588P
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                (DOWN/) DOWNS D. (GRAL/) GRALNICK J A.
                                                                                                                                                                                                                                                                                              US2002072118-A1
                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                             05-NOV-2002
                                                                                                                                                                                                                                                                                                                           13-JUN-2002
 61
                                                                                                                                ABB78154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Downs D,
                                                                          RESULT 19
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                                                                                         ABB78154
                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YgdX protein (a protein identified from Salmonella enterica servora typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YgdX reduces the oxidation of [Fe-8] clusters, and thus reduces the loss of Fe[II] ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for
                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                   Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                   1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                     1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          superoxide damage in a bacterial, yeast, mammalian or plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.7%; Score 373; DB 5; Length 87; 75.9%; Pred. No. 4e-35;
                                             Length 87;
                                        ; Score 379; DB 5; Length 87; Pred. No. 8.1e-36; 14; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a YggX homologue.
                                                                                                                                                                              EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                 ABB78153 standard; protein; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 1A; 16pp; English.
                                           78.0%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-2001; 2001US-00955502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-2000; 2000US-0234588P
                                                                        66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DOWN/) DOWNS D.
(GRAL/) GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Downs D, Gralnick JA;
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Best Local Similarity
66; Conserve
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                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002072118-A1.
                Sequence 87 AA;
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                                                                                                                                                                                                                                                                                                                           05-NOV-2002
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                                                                                                                                                                                                                                                                                              ABB78153;
                                          Query Match
Best Local
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                                                            Best Loc
Matches
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                                                                                                                           plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                           specification describes a method for reducing superoxide damage
                                                                                                                  Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
68.3%; Score 332; DB 5;
Best Local Similarity 68.2%; Pred. No. 2.3e-30;
Matches 60; Conservative 12; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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Gralnick JA;
                                                       WPI; 2002-589476/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 88 AA;
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plant a

(first entry)

05-NOV-2002

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cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterios serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIWQQISKEAWEEWKQIQTRLVNENRLNLADA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                          specification describes a method for reducing superoxide damage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSRTIFCTFLOREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%; Score 255; DB 5; 55.2%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RARKYLOQOMERFLFEDGTVEAQGYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB78147 standard; protein; 87 AA.
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                                        18-SEP-2001; 2001US-00955502
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                                                                               22-SEP-2000; 2000US-0234588P
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Best Local Similarity 55.2
Matches 48; Conservative
                                                                                                                                                                                   Gralnick JA;
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                                                                                                                         DOWNS D. GRALNICK J A.
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GRALNICK J A.
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13-JUN-2002
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(GRAL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification describes a method for reducing superoxide damage to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                            Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reducing superoxide damage in a bacterial, yeast, mammalian or plant
cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 265; DB 5; Length 76; Pred. No. 1.1e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 54.5%; Score 265; DB Local Similarity 61.8%; Pred. No. 1.1e es 47; Conservative 16; Mismatches
                                        Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a YggX homologue.
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English.

Example; Fig 1A; 16pp;

18-SEP-2001; 2001US-00955502 22-SEP-2000; 2000US-0234588P

US2002072118-A1

13-JUN-2002

Unidentified

Gralnick JA, DOWNS D. GRALNICK J A.

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( /NIMOD) (GRAL/) Downs WPI; 2002-589476/63.

ABB78148 standard; protein; 87 AA.

RESULT 21 ABB78148 (first entry)

05-NOV-2002

ABB78148;

Bordetella parapertussis

US2002072118-A1

61 EHRKLLEQEMVNFLFE 76 ||||| :|: | |||: EHRKKIEKYMKLFLFK 76

Sequence 76 AA;

Query Match

Matches

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where the cells are

9 9

84

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0; Gaps

Length 86; 25; Indels

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The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L.
                   rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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                                                                                                                                                                                                                                                                                                                                                1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWQHKOTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Etienne J, Ma L, Cazalet C,
Zidane N, Magnier A, Kunst F,
                                                                                                                                                                                                                                ch
    49.6%; Score 241; DB 5;
1 Similarity 54.8%; Pred. No. 7.7e-20;
46; Conservative 13; Mismatches 25
serovar typhimurium) or its homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; infection; Antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 5908; 660pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L. pneumophila protein SEQ ID NO 5908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE & RECH
(UYLY-) UNIV LYON 1 BERNARD CLAUDE.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RARKYLQQQMERFLFEDGTVEAQG 84
                                                                                                                                                                                                                                                                                                                                                                                                                     61 EHRKLLEQEMVNFLFEGKEVHIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB41576 standard; protein; 89
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Rusniok C, Bouchier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legionella pneumophila
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2005049642-A2.
                                                                                                                                                                                       Sequence 86 AA;
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Jarraud S;
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                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                     cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Re-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant
                                             Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIWQQISKEAWEEWKQIQTRLVNENRLNLADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                       specification describes a method for reducing superoxide damage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%; Score 255; DB 5; Length 87; 55.2%; Pred. No. 1.9e-21; tive 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a YggX homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RARKYLQQQMERFLFEDGTVEAQGYVP
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                                                                                                                                          Example; Fig 1A; 16pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 1A; 16pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2001; 2001US-00955502
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Les 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 87 AA;
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셤 ઠે g Glaser P; Vandenesch F;

The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella

MEDICALE

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The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful a primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a L. pneumophila protein.
                                                                                                                                              1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA 60
                                                                                                                                                                Glaser P;
Vandenesch F;
 pneumophila. The present squence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the strain and for treatment and prevention of infections.
                                                                                                                 Gaps
                                                                                                                 ij
                                                                               Length 89;
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Zidane N, Magnier A, Kunst F,
                                                                                                                 Indels
                                                                             47.6%; Score 231.5; DB 9;
53.8%; Pred. No. 1e-18;
ive 17; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection; infection; Antibacterial; Vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                L. pneumophila protein SEQ ID NO 2626.
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                                                                Query Match
Best Local Similarity 53.0.
Best Local 43; Conservative
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                L. pneumophila protein.
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                                                 Sequence 89 AA;
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Jarraud S;
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Sequence 95 AA;

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                                                                              1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                               ;;
                 Length 95;
                                               Indels
              47.6%; Score 231.5; DB 9;
53.8%; Pred. No. 1.1e-18;
cive 17; Mismatches 19;
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67 RAREFLKEEMQKYFFGEGSE 86
Query Match
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Search completed: June 27, 2007, 11:04:47 Job time: 219 secs

naemophilus vibrio fisc pseudoalter

shewanella shewanella shewanella shewanella

shewanella

Run on:

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PubMed=16275786; DOI=10.1093/nar/gki954;
Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu. Xu., Sun L., Chen S.,
Wang J., Xiong Z., Dong J., Xue Y., Yan Y., Yan Z., Wan J., Chen S.,
Wie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
Qiang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery.";
Nuclaic Acids Res. 33:645-6458 (2005).
-!- FUNCTION: Could be a mediator in iron transactions between iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2006, entry version 7.
Probable Fe(2+)-trafficking protein.
Name-yggx, OrderadLocusNames=SBO 3028;
Shigella boydii serotype 4 (strain Sb227).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteria, Enterobacteria, Namespeckeria, Britario 300268;
NTB_TAXID=300268;
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11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
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                                                                                                        Q3P4C9_9GAMM
Q2Z5M4 9GAMM
Q2Z5M5_9GAMM
Q368P1_9GAMM
PETP_IDILO
Q3NME3_SHBPR
PETP_SHEON
PG1FVU6_9GAMM
PETP_COLP3
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Q1ZF27 9GAMM
Q1LSZ8 BAUCH
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                                                 030,077 9GAMM
033073 9GAMM
022RK9 SHEPU
0307K0 9GAMM
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1 MSRTIFCTFLQREAEGQDFQ......NFLFEGKEVHIEGYTPEDKK
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Q65vt7
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            GenCore version 6.2.1 (c) 1993 - 2007 Biocceleration Ltd.
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Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Result

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0.2 c 312 0.5 c 712 0.3 d 73 0.3 d 73 0.3 d 73 0.3 d 74 0.3 d 89 0.4 d 80 0.5 c 10 0

blochmannia dechloromon

wiggleswort

rhodoferax legionella

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bordetella

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methylobaci

pseudomonas pseudomonas

Q48c72 Q87uf5 Q4z1p3 09pc73 088r49

colwellia p psychromona buchnera ap

psychromona pseudoalter baumannia c

shewanella shewanella

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shewanella

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ProDom; PD029191; DUF495; 1.
                          Complete proteome; Iron.
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                                                                                               SEQUENCE
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                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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  acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Mang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
Nie H., Peng J., Xu J., Wang Y., Yann Z., Wen Y., Yao Z., Shen Y.,
Ganome dynamics and diversity of Shigella species, the etiologic
"Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
Nucleic Acids Res. 33:6445-6458(2005)
-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/o
repair of Pe-S clusters in biosynthetic enzymes (By similarity).
-!- SUBUNIT: Monomer (By similarity)
                                               -!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the Pe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable Fe(2+)-trafficking protein.
Name-yggX; OrderedLocusNames=SDY 3110;
Shigella dysenteriae serotype 1 (atrain Sd197).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterials.
Enterobacteriaceae; Shigella.
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/FTId=PRO_0000246116.
1E3625B77C32B94B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 486; DB 1;
100.0%; Pred. No. 7.3e-42;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                   HAMAP, MF 00686; -; 1. —
InterPro; IPR007457; YggX.
Pfam, PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
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GenomeReviews; CP000036_GR; SBO_3028
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                                                                                                                                                                                                                                                                                                                                                                                                                                             91 AA; 10953 MW;
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                                                                                                                                                                                                                                                                                                                                                                        Complete proteome; Iron.
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Q32C31;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agents of bacillary dysentery.";
Nucleic Acids Res. 33:6445-6458(2005).
-1- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or
                                                                                                                                                                                                                                                                             1 MSRIIFCIFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNA
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-!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=16275786; DOI=10.1093/nar/gki954;
Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
"Genome dynamics and diversity of Shigella species, the etiologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiqella sonnei (strain Ss046). —
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
Probable Fe(2+) -trafficking protein.
/FTId=PRO 0000246117.
1E3625B77C32B94B CRC64;
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                                                                                                       ; Score 486; DB 1; Length 91;
; Pred. No. 7.3e-42;
0; Mismatches 0; Indels
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1E3625B77C32B94B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA.
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InterPro; IPR07457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
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GenomeReviews; CP000038_GR; SSO_3234
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                                                                                                                      100.08;
                                                              91 AA; 10953 MW;
                                                                                                                                                 100.0%;
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                                                                                                                                        Local Similarity 100.
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Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of genes subject to positive selection in uropathogenic strains of Escherichia coli: A comparative genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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STRAIN-0157-117 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; Pubmed=11206551; DOI=-10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 486; DB 2; Length 91; 100.0%; Pred. No. 7.3e-42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91. AA; 10953 MW; 1E3625B77C32B94B CRC64;
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                                                                                                                                                                                                                                                               16-MAY-2006, integrated into UniProtKB/TrEMBL. 16-MAY-2006, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=16585510; DOI=10.1073/pnas.0600938103;
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Name=yggX; OrderedLocusNames=Z4307, ECs3838;
Escherichia coli 0157:H7.
                                                                                                                                                                                                      91 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CP000243; ABE08801.1; -; Genomic_DNA
HHKLLEQEMVNFLFEGKEVHIEGYTPEDKK
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Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                              11-JUL-2006, entry version 4.
Hypothetical protein yggx.
Hypethetical protein yggx.
Bscherichia coli (strain ŪT189 / UPEC)
                                                                                                                                                                                                   PRT;
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Q1R763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
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                                                                                                                                                                                                                                                                                        STRAIN=0157:H7 / Sakai / RIMD 0509952 / BHEC;
MEDLINE=21156231; PubMed=11258795; DOI=10.1093/dnares/8.1.11;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinaqawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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Probable Fe(2+)-trafficking protein.
/FrId=PRO_0000214479.
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
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Pred. No. 2.3e-41;
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EMBL; BA000007; BAB37261.1; -; Genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenomeReviews; BA000007 GR; EC838
GenomeReviews; AE005174 GR; Z4307
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Best Local Similarity 100.
Matches 90; Conservative
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PIR; F91108; F91108.
SMR; POA8P4; 1-90.
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EchoBASE; EB2809;
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DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
DOI=10.1018kis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
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-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Pe-S clusters in biosynthetic enzymes. Necessary to
                   MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331:1453; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003; Pomposiello P.J. Koutsolioutsou A., Carrasco D., Demple B., "SoxRS-regulated expression and genetic analysis of the yggX gene Escherichia coli.";
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-!- SUBUNIT: Monomer (Probable).
-!- INDUCTION: By oxidative stress and soxs.
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wasinger V.C., Humphery-Smith I.; "Small genes/gene-products in Escherichia coli K-12."; FEMS Microbiol. Lett. 169:375-382(1998).
                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                 STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;
DOI=10.1038/msD4100049;
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EMBL; U00096; AAC75999.1; -; Genomic_DNA.
EMBL; AP009048; BAE77025.1; -; Genomic_DNA.
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STRAIN=K12 / MG1655 / ATCC 47076;
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                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL PROTEIN SEQUENCE OF 1-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
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PDB; 1YHD; NMR; A=1-90.
SWISS-2DPAGE; POA8P3; COLI.
GenomeReviews; U00096_GR; b2962.
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                        3D-structure; Complete proteome; Direct protein sequencing; Iron. O CHAIN 1 90 Probable Fe(2+)-trafficking protein.
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Enterobacteriaceae, Shigella.
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DO1=10.1128/IAI.7115.2775-2786.2003;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
                                                                                                                                                                                                               Probable Fe(2+)-trafficking protein
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POABE; PS2065;
POABE; PS2065;
O7-UNV-2005, integrated into UnibrotKB/Swiss-Prot.
07-JUN-2005, sequence version 1.
PS-JUL-2006, entry version 12.
Probable Fe (2+) -trafficking protein.
Name-yggX; OrderedLocusNames=SF2959, S_3162;
                                                                                                                                                                                                                                           /FTId=PRO 0000214478
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Pred. No. 2.3e-41;
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STRAIN=ATCC 700930 / 2457T / Serotype 2a;
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                        HAMAP; WF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
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EcoGene; EG12984; yggX
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PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15781495;
PubMed=15.
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRTIFCTFLOREABGODFOLYPGELGKRIYNBISKEAWAOWOHKOTMLINBKKLNWMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNWMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
Probable Fe(2+)-trafficking protein.
/FTId=PRO_0000214502.
                                                                                                                                                                                                                                                                                                                                                              By similarity.
Probable Fe(2+)-trafficking protein.
/FTId=PRO_0000214480.
D7C66C2A35E63692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2005, integrated into UniProtKB/Swiss-Prot. 19-JUL-2005, sequence version 2. 11-JUL-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 477; DB 1;
Pred. No. 6e-41;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HRKILEQEMVNFLPEGKEVHIEGFTPEDKK 90
                                                                                   EMBL; AE014075; AAN81998.1; -; Genomic_DNA
SMR; Q8FE19; 1-90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                                                                                                                                         GenomeReviews, AR014075 GR; c 3550.
Blocyc, RC0L199310:03550-MONOMER; -.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron,traffic; 1.
Pfam; PF04362; Iron,traffic; 1.
Prop; PIRSF; PIRSF029877; Fe traffic_YggX; 1.
ProbOm; PD029191; DU07495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=yggX; OrderedLocusNames=SCH_3052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenomeReviews; AE017220_GR; SCH_3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable Fe(2+)-trafficking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00686; -; 1.
InterPro; IPR007457; Y9gX.
Pfam; PP04362; Iron traffic; 1.
ProDom; PD029191; DUP495; 1.
Complete proteome; Iron.
INIT MET 0 0 By si
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 AA; 10805 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.9
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella choleraesuis.
                                                                                                                                                                                                                                                                                                                                       Complete proteome; Iron INIT MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
  Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella (Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLANWANAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                -!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the Pe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 0 By similarity.
1 90 Probable Fe(2+)-trafficking protein.
FTId=FRO 0000214597.
90 AA; 10821 MW; D7C66C2A\(\begin{array}{c} \frac{1}{2}\) SE62402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-JUL-2003, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE005674; AAN44440.1; -; Genomic_DNA.
EMBL; AE014073; AAP18264.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenomeReviews; AE014073_GR; S_3162.
GenomeReviews; AE005674_GR; SF2959.
HAMAD: MF 00686; -; 1.
INTERPRO; IPR007457; YggX.
Pfam; PP64362; Iron traffic; 1.
PIRSF; PRRSF029877; Petraffic; 1.
PRODOM; PD029191; DUP495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUL-2003, sequence version 2.
11-JUL-2006, entry version 21.
Probable Re(24)-trafficking protein.
Name=yggX; OrderedLocusNames=c_3550;
Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Iron. INIT MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014073; AA
SMR; P0A8P5; 1-90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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        RAARTHARTA BAARA B
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 700931 / Ty2;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB1.185.7.2330-2337.2003;
Doil-10.1128/JB1.185.7.2310-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in synthetic enzymes (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SRIIPCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNNMNAE
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Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B3B6A1EE22555E3C CRC64;
                                                                                                                                                   P67618; Q8XFV6;
11-0CT-2004, integrated into UniProtKB/Swiss-Prot.
11-OCT-2004, sequence version 1.
11-JUL-2006, entry version 14.
Probable Fe(2+)-trafficking protein.
Name-yggX; OrderedLocusNames-STY3266, t3024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 464; DB 1;
Pred. No. 1.3e-39;
5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                   90 AA.
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EMBL; AE014613; AAO70576.1; -; Genomic_DNA.
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PP04362; Iron_traffic; 1.
PIRSF; PIRSF02982; Fe_traffic_YggX; 1.
PRODOM; PD029191; DUP495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenomeReviews; AL513382_GR; STY3266.
GenomeReviews; AE014613_GR; t3024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 AA; 10768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Conservative
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Iron. INIT MET 0 0
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                                                                                                                                                                                                                                                                                          Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=601;
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                                                                                          RESULT 11
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                                                                                                                                   2 SRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or
                                                                                                                                                            SRTIFCTYLORDAEGODFOLYPGELGKRIYNEISKDAWAOWOHKOTWLINEKKLANWANAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Clifton S.W., Latreille P., Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid.";

Nat. Genet 36:1268-1274(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRTIFCTYLORDAEGODFOLYPGELGKRIYNEISKDAWAQWQHKQTWLINEKKLNNMNAE
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                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repair of Fe-S clusters in biosynthetic enzymes (By similarity). SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
Probable Fe(2+)-trafficking protein.
/FTId=PRO 0000214503.
B3B6A1EEZ2555E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                 Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 464; DB 1; Length 90;
Pred. No. 1.3e-39;
                                                        1.3e-39;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
    10768 MW; B3B6A1EE22555E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
                                                 Score 464; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                90 AA
                                                                   k; Pred. No. 1.3e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                               HRKLLEQEMVSFLFEGKDVHIEGYTPEDKK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
                                                                                                                                                                                                                         HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 HRKLLEQEMVNFLPEGKEVHIEGYTPEDKK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2006, entry version 11.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=SPA2974;
Salmonella paratyphi-a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 9150 / SARB42;
PubMed=15531882; DOI=10.1038/ng1470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenomeReviews; CP000026_GR; SPA2974.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2005, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00686; -; 1. —
InterProc; IRR007457; YGgX.
Pfam; PF04362; Iron traffic; 1
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 AA; 10768 MW;
                                                                   94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.5%;
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                                      Query Match
Best Local Similarity 94.44
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Conservative
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    90 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=54388;
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OSPMM1:
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    SEQUENCE
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PubMed=15516576; DOI=10.1128/JB.186.22.7626-7634.2004;
PubMed=15516576; DOI=10.1128/JB.186.22.7626-7634.2004;
Skovram B., Lauthon C.T., Downs D.M.;
Lack of YggX results in chronic oxidative stress and uncovers subtle defects in Fe-S cluster metabolism in Salmonella enterica.";
J. Bacteriol. 186:7626-7634(2004).
-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes. Necessary to maintain high levels of aconitase under oxidative stress.
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
SRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINEKKLNMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gralnick J.A., Downs D.M.;
"Protection from superoxide damage associated with an increased level
"Ortice YGAX protein in Salmonella enterica.";
Proc. Natl. Acad. Sci. U.S.A. 98:8030-8035(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trafficking and minimizes the DNA damage caused by hydroxyl radicals: residue Cys-7 is essential for YggX function."; J. Biol. Chem. 278:20708-20715(2003).
                                                                                                                                                                                                                                                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Coutrney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R., Wilson R.K.; "" "" "Waterston R. Waterston R. Waterston Removar Typhimurium
                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pubbled=12670952; DOI=10.1074/jbc.M301577200;
Gralnick J.A., Downs D.M.;
"The YggX protein of Salmonella enterica is involved in Fe(II)
                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
                                                                                                                                                  P67617; QBXFV6;
11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
11-OCT-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11416172; DOI=10.1073/pnas.151243198;
                                                                                                                                        90 AA
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PDB; 1XS8; NMR; A=1-90.
                                               61 HRKLLEQEMVSFLPEGKDVHIEGYTPEDKK 90
                               HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                                                                                                                                                                                                              Probable Fe(2+)-frafficking protein.
Name-yggX; OrderedLocusNames=STW3111;
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenomeReviews; AE006468_GR; STW3111.
StyGene; SG7777; yggX.
HAMAD; MF_00686; -1 1.
InterPro; IPR001457; yggX.
Pfam; PF04362; Iron_traffic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND MUTAGENESIS OF CYS-6
                                                                                                                                        PRT;
                                                                                                                                                                                                   11-JUL-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                         NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LT2;
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                                                                                                                                        SALTY
                                 62
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FETP_SALTY
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Pe-S clusters in biosynthetic enzymes (By similarity).
-!- SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRTIFCTYLORDAEGODFOLYPGELGKRIYNEISKDAWAOWOHKOTMLINEKKLNMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

    SUBUNIT: MONOMET (By SIMILATILY).
    SIMILARITY: Belongs to the Pe(2+)-trafficking protein family.

                     Probom; P0029191; DUF495; 1.
3D-structure; Complete proteome; Iron.
INIT MET 0 0 By similarity.
CHAIN 1 90 Probable Pe(2+)-trafficking protein.
                                                                                                                          /riid=rko_u000214505.
C->S: Strong decrease in activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                 /FTId=PRO 0000214505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 464; DB 1;
Pred. No. 1.3e-39;
5; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 HRKLLEQEMVSFLFEGKDVHIEGYTPEDKK 90
PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2006, entry version 13.
Probable Fe(2+)-trafficking protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.5%;
94.4%;
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Best Local Similarity 94...
Local Similarity 94...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Score 402; DB 1;
Pred. No. 3e-33;
7; Mismatches
                                                                                                                                                                                                                                                                                                              90 AA
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GenomeReviews; AE003852_GR; VC0451.
TIGR; VC0451; -
                                                          8; Mismatches
                                                                                                                                                                                                61 EDRKLLEQEMVNFLFEGODVHIAGYTPPSK 90
                                                                                                                                                                          61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
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InterPro; IPR007457; YggX.
Pfam; PP09362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Probable Fe(2+)-trafficking protein
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2006, entry version 23.
                    83.1%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=VC0451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483 (2000).
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Best Local Similarity 83.3.
Best Local 5; Conservative
                  Query Match 83.1
Best Local Similarity 83.3
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
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FETP_VIBCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                  1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNA
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repair of Fe-S clusters in biosynthetic enzymes (By similarity). SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                          Probable Fe(2+)-trafficking protein.
/FTId=PRO 0000214481.
9B295D34B542D8A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the Pe(2+)-trafficking protein family.
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/FTId=PRO 0000214520.
C7375E7954752E64 CRC64;
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                                                                                                                                                                                                                                                                    Score 411; DB 1; Length 90;
Pred. No. 3.5e-34;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA.
                                                                                                                                                                                                                                                                                                            6; Mismatches
                    EMBL; BX950851; CAG73886.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BX936398; CAH22463.1; -; Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DDRKLLEQEMIKFLFEGKDVHIEGYTP 87
                                                                          Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                61 EHRKLLEQEMVNFLFEGKEVHIEGYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMR; Q666M3; 1-90.
GenomeReviews; BX936398_GR; YPTB3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2004, sequence version 1.
11-JUL-2006, entry version 13.
Probable Fe(2+)-trafficking protein.
                                                          GenomeReviews; BX950851_GR; ECA0975
                                                                                                                                                                                                                                  90 AA; 10640 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 AA; 10608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pseudotuberculosis.
                                                                                                                                                                                                                                                                      Match 84.6%;
Local Similarity 87.4%;
es 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=YPTB3225;
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InterPro; IPR007457; YggX
                                                                                                                                                                            Complete proteome; Iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                8
                                          Q6D8J9; 1-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=633;
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                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q666M3;
                                                                                                                                                                                              CHAIN
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ID FETP 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic ensymes (By similarity).
-i- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                        1 MSRTIFCTFLKKDAEGODFQLYPGEIGKRIYNEISKEAWSQWITKQTWLINEKKLSMMNI
                                                                                                                                                            1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWQTKQTWLINEKKLNMMDP
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                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WICTROTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-ATCC 39315 / El Tor Inaba Ni6961 / Serotype 01;
MEDLINE-20406833; PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Gill S.R., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson R.E., Read T.D., Tettellin H., Richardson D.L., Sermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Bragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., McMealanos J.J., Venter J.C., Praser C.M., Smith H.O., Colwell R.R., "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable Fe(2+)-trafficking protein.
/FTId=PRO 0000214508.
972331B2600B3184 CRC64;
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Vibrionaceae; Vibrio.
Score 404; DB 1; Length 90;
Pred. No. 1.9e-33;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 90;
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00686; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                 Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
-!- SIMILARITY: Belongs to the Pe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pubmed=14656965; DOI=10.1101/gr.1295803;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-Y., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probable Pe(2+)-trafficking protein.
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Choy H.E.;
                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 402; DB 1; Length 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
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7EA0CB75840A255C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2004, integrated into UniProtXB/Swiss-Prot.
                                                                                                                                 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE016795; AA009940.1; -; Genomic_DNA.
GenomeReviews; AE016795 GR; VVI 1514.
BioCyc; VVUL216895:VV11514-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EHRKLLETEMVNFLFEGKEVHIEGYTPPSK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
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                                                                                                                                                                            11-JUL-2006, entry version 19.
Probable Fe(2+)-trafficking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=VV2885; Vibrio vulnificus (strain YJ016).
                                                                                                                                                          , sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00686; -; 1.
InterPro.; IFR007457; YGGX.
Pfam; PF04362; Iron_traffic; 1.
Probom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry version 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AA; 10614 MW;
                                                                                                                                                                                                                         OrderedLocusNames=VV1_1514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Conservative
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                                                                                      STANDARD;
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                                                                                                                                                                                                                                           Vibrio vulnificus.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=672;
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                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CMCP6
                                                          FETP_VIBVU
ID FETP_VIBVU
AC Q8DCC5;
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Q7MHI4;
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ID FETP V
DT 10-MAY
DT 10-MAY
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DE PROBLE
GN ORGER
OC BACTER
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                   Genome Res. 13:2577-2587(2003).
-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Re-S clusters in biosynthetic enzymes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic ensymes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRITVPCARLNKEADGLDFQLYPGELGKRIFDNISKEAWGQWQHKQTMLINEKKLNMMDP
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MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Kubota A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable Fe(2+)-trafficking protein... /FTId=PRO 0000214512. 7EA0CB75840A255C CRC64;
                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; "Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 402; DB 1;
Pred. No. 3e-33;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BA000037; BAC95649.1; -; Genomic_DNA. GenomeReviews; BA000037 GR; VV2885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BA000031; BAC60890.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EHRKLLETEMVNFLFEGKEVHIEGYTPPSK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biocyc; VVUL196600:VV28B5-MONOMER; -. HAMAP; MF_00686; -; 1. InterPro; IPR004857; YggX. Pfam; PF04356; Iron_traffic; 1. PRSF; PIRSF029827; Fe traffic_YggX; 1. ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
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Probable Pe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenomeReviews; BA000031_GR; VP2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 AA; 10614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=VP2627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 82.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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STANDARD;

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sioCyc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSRIVFCARLKKEGEGLDFQLYFGELGKRIFDNISKEAWAQWQHKQTMLINEKKLNMMDP
                                                                                                                                                                                           1 MSRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                 Gaps
                                                                         Probable Fe(2+)-trafficking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2006, sequence version 1.
11-MIL-2006, entry version 3.
Hypothetical protein.
ORFNames-V12601 14084,
Vibrio alginolyFicus 12601.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                              Score 399; DB 1; Length 90;
Pred. No. 6e-33;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 397; DB 2; Length 90;
Pred. No. 9.7e-33;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=12G01;
Polz M., Ferriera S., Johnson J., Kravitz S., Halpern A.,
Remington K., Beeson K., Tran B., Rogers Y.-H., Friedman l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
Submitted (MAR-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                         /FTId=PRO 0000214510.
A20D59535F0F9A1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l protein.
90 AA; 10629 MW; A75D0C535F0F9A1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AAPS01000056; EAS74087.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-2006, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                        90 AA
                                                                                                                                                                                                                                                    61 EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
                                                                                                                                                                                                                                                                   61 EHRKILETEMVNFLFEGKDVHIEGYTP 87
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InterPro, IPR007457; YggX.
Pfam, PP094362; Iron_traffic, 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
Probom; PD029191; DUP495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007457; YggX.
Pfam; PPG4362; I. Iron Lraffic; I.
PIRSF; PTRSF029827; Pe traffic_YggX; 1.
ProDom; PD029191; DUP495; I.
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                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                     90 AA; 10629 MW;
                                                                                                                                   82.1%;
83.9%;
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Local Similarity 82.8%;
es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                               Local Similarity 83.9
Les 73; Conservative
                                                             Complete proteome; Iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=314288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q1V3X2; 1-87
                                                                                                                                                                                                                                                                                                                                                   QIV3X2_VIBAL
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SEQUENCE 90
                                                                                                      SEQUENCE
                                                                                                                                   Query Match
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Matches
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FETP\_YERPE

RESULT 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOI=10.1128/JB.19.4.16.4601-4611-24.00;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                   MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083; MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083; MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083; Maren B.W. Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D., Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z., Jin L., Dai R., Chen P., Li S., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.; "Complete genome sequence of Yershinia pestis strain 91001, an isolate avirulent to humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable Fe(2+)-trafficking protein.
/FTId=PRO_0000214519.
                                         25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=91001 / Biovar Mediaevalis;
PubMed=15368893; DOI=10.1093/dnares/11.3.179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ414145; CAC89796.1; -; Genomic_DNA.
EMBL; AE009952; AAM86890.1; -; Genomic_DNA.
EMBL; AE017140; AAS63643.1; -; Genomic_DNA.
SNR; QEZHE7; 1-90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                                  Probable Fe (2+) -trafficking protein.
OrderedLocusNames=YP00953, y3340, YP3488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Monomer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenomeReviews; AE017042 GR; YP3488.
GenomeReviews; AL590842 GR; YP00953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenomeReviews; AE009952_GR; y3340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPES187410: Y3340-MONOMER;
                                                               , sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPES632: YPO0953-MONOMER;
                                                                                 entry version 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONA Res. 11:179-197 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BioCyc, YPES632:YP00953-MC
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:523-527(2001).
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                                                                                                                                                 fersinia pestis.
                                                                                                                                                                                                              NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                      US DOB Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C.,
Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
Chain P., Hu P., Malfatti S.A., Radnedge L., Vergez L.M., Larimer F.,
Land M., Hauser L., Worsham P., Chu M.C., Andersen G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive genome erosion and functional adaptations provide insights into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 16:149-156(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodalis glossinidius (strain morsitans).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                         Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                            Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
Vergez L.M., Worsham P., Chu M.C., Andersen G.L.;
"Complete Genome Sequence of Yersinia pestis Strains Antiqua and
Nepal516: Evidence of Gene Reduction in an Emerging Pathogen.";
J. Bacteriol. 188:4453-4463 (2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pestis Antiqua.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=16365377; DOI=10.1101/gr.4106106;
Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
Hattori M., Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein.
90 AA; 10707 MW; C7374E6855653F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
07-PEB-2006, sequence version 1.
25-JUL-2006, entry version 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 396; DB 2; L
Pred. No. 1.2e-32;
8; Mismatches 8;
11-JUL-2006, integrated into UniProtKB/TrEMBL.
11-JUL-2006, sequence version 1.
11-JUL-2006, entry version 1.
Hypothetical protein:
ORFNames=YPA_0311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of chromosome of Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; CP000308; ABG12279.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDRKLLEQEMVNFLFEGODVHIAGYTPPSK 90
                                                                                                                                                                                                                       STRAIN=Antiqua;
PubMed=16740952; DOI=10.1128/JB.00124-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-2006, entry version 6.
Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                           Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%;
82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Sodalis.
                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=SG2036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 82.2
74; Conservative
                                                                                                      Yersinia pestis Antiqua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                NCBI_TaxID=360102
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Antiqua;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q2NRB4;
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FETP_SODGM
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      쉽
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                                                                                                                                                                  1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKKLSMMNI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                             1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNNMMNA
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Nepaisis;
US DOB Joint Genome Institute;
US DOB Joint Genome Institute;
Barry K., Lucas S., Lapidus A., Copeland A., Detter J.C.,
Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
Chain P., Hu P., Malfatti S.A., Radnedge L., Vergez L.M., Larimer I
Land M., Hauser L., Worsham P., Chu M.C., Andersen G., Richardson I
"Complete sequence of Chromosome of Yersinia pestis Nepaision Submitted (APR-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis Nepal516.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Nepal516;
PubMed=16740952; DOI=10.1128/JB.00124-06;
Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
Vergez L.M., Worsham P., Chu M.C., Andersen G.L.;
"Complete Genome Sequence of Yersinia pestis Strains Antiqua and
Nepal516: Evidence of Gene Reduction in an Emerging Pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                      ;
                                                           Score 396; DB 1; Length 90;
Pred. No. 1.2e-32;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 396; DB 2; Length 90;
Pred. No. 1.2e-32;
8; Mismatches 8; Indels
    R -> G (in Ref. 3).
C7374E6855653F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2006, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; CP000305; ABG19478.1; -; Genomic_DNA.
                                                                                                      8; Mismatches
                                                                                                                                                                                                                                              61 EDRKILEQEMVNFLFEGODVHIAGYTPPSK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BDRKLLEQEMVNFLFEGODVHIAGYTPPSK 90
                                                                                                                                                                                                                           EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
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                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 188:4453-4463 (2006).
                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2006, sequence version 1.
      16 16
90 AA; 10707 MW;
                                                           Query Match
Best Local Similarity 82.2%;
Matches 74; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%;
82.2%;
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=377628;
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QICB93 YERPE
QICB93;
                                                                                                                                                                                                                                                                                                                                                               QICEV2_YERPE
Q1CEV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
    CONFLICT
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Matches

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RESULT 22

Q1CB93 ID Q1 AC Q1

9 9

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Length 90; Indels

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FETP HAEI8
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             SEQUENCE
                                                                                                                                                                                                                                                    Q4QMD9;
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FETP_HAEI8
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                                                                                                                                                                                                                                                                                                                                                    1 MSRTIYCTFLKREAEGQDFQFYPGELGKRIYDNISKEAWTQWQTKQTMLINEKKISMMVV 60
                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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acquisition and iron-requiring processes, such as synthesis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                    1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWOHKOTMLINEKKLNMMNA
            repair of Fe-S clusters in biosynthetic enzymes (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Could be a mediator in iron transactions between iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15378067; DOI=10.1038/nbt1010; Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K., Kim C.H., Jeong H., Hur C.G., Kim J.J.; "The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens.";
                                                                                                                                                                                                                           Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable Fe(2+)-trafficking protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannheimia succiniciproducens (strain MBEL55E).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                              Score 390; DB 1; Length 90;
Pred. No. 5.1e-32;
                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                      /FTIG=PRO 0000246119.
90 AA; 10701 MW; E9016C38ASD05394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA
                                                                                                      EMBL; AP008232; BAE75311.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016827; AAU36923.1; -; Genomic_DNA
                                                                                                                                           HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PP04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                       61 EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
                                                                                                                                                                                                                                                                                                                                                                                                       61 ADRKVLEQEMINFLFEGQDVHIQGYTP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenomeReviews; AE016827_GR; MS0316.
HAWAP; MF 00686; -; 1.
InterPro; IRR00485; Y9gX.
Pfam; PF04362; Iron traffic; 1.
PIRSE; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable Fe(2+)-trafficking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Biotechnol. 22:1275-1281(2004)
                                                                                                                               GenomeReviews; AP008232_GR; SG2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry version 12
                                                                                                                                                                                                                                                                                80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=MS0316;
                                                                                                                                                                                                                                                                                                         70; Conservative
                                                                                                                                                                                                                Complete proteome; Iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=221988;
                                                                                                                    SMR; Q2NRB4; 1-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMR; Q65VT7; 1-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FETP MANSM
                                                                                                                                                                                                                                                       SEQUENCE
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FETP_MANSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 187:4627-4636(2005).
-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                        1 MARTVFCEYLKKEABGLDFQLYPGELGKRIFDSVSKQAMGEWIKKQTMLVNEKKLNMMNA
                                                                                                                                                                                              1 MSRIIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence of an otitis media isolate of nontypeable
Haemophilus influenzae: comparative study with H. influenzae serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRIIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Pubmed=15968074, DOI=10.1128/JB.187.13.4627-4636.2005;
Harrison A., Dyer D.W., Gillaspy A., Ray W.C., Mungur R., Carson Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales;
Pasteurellaceae, Haemophilus.
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Pest Local Similarity 78.2%; Pred. No. 1e-31;
Matches 68; Conservative 12; Mismatches 7; Indels
                                                                             Length 91;
                                                                                                                                       Indels
                         8190E2DAOB35AACC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=PRO 0000246101.
EB34CEFF7737B93B CRC64;
/FTId=PRO_0000214489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrated into UniProtKB/Swiss-Prot
                                                                             80.0%; Score 389; DB 1; 78.4%; Pred. No. 6.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 AA.
                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CP000057; AAX87808.1; -; Genomic_DNA.
SMR; Q4QMD9; 1-87.
                                                                                                                                                                                                                                                                                                         61 EHRKLLEQEMVNFLFEGKEVHIEGYTPE 88
                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae (strain 86-028NP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
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HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2006, integrated into Uni:
19-JUL-2005, sequence version 1.
                         91 AA; 10801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AA; 10582 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry version 7
                                                                          Query Match
Best Local Similarity 78.4%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=NTHI0920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome; Iron.
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J. Bacteriol. 187:
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Munson R.S. Jr.;
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Search completed: June 27, 2007, 11:10:39 Job time: 349 secs

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TYPE: PRT; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962
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Sequence 11962, A
Sequence 5443, Ap
Sequence 23355, A
Sequence 2855, Ap
Sequence 2859, Ap
Sequence 3, Appli
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                                                                                                                           June 27, 2007, 11:10:57; Search time 50 Seconds (without alignments) 159.306 Million cell updates/sec
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1: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/5_COMB.pep:*
2: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/6_COMB.pep:*
3: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/1_COMB.pep:*
4: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/H_COMB.pep:*
5: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/H_COMB.pep:*
5: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/RE_COMB.pep:*
7: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/RE_COMB.pep:*
7: \times_EMC_Celerra_SIDS3/\text{ptodata}/2/iaa/RE_COMB.pep:*
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Copyright (c) 1993 - 2007 Biocceleration Ltd.
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 1004, Ap
Sequence 934, Appl
Sequence 934, Appl
Sequence 4802, Ap
Sequence 4800, Ap
Sequence 6012, Ap
Sequence 11703, A
Sequence 48, Appl
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Sequence 18911, A
Sequence 12, Appl
Sequence 6879, Ap
Sequence 2850, Ap
Sequence 2850, Ap
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Sequence 205, App
Sequence 6400, Ap
Sequence 41746, A
Sequence 46116, A
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42959, A
5, Appli
8, Appli
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6689, Ap
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Sequence 61671, A
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Sequence 22
Sequence 66
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US-09-914-098-46
US-09-328-352-5836
US-09-252-991A-20905
US-09-270-767-58283
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S-09-134-000C-4346
S-09-248-796A-18911
S-09-861-451A-12
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S-09-248-796A-19555
S-09-710-279-2850
S-09-134-001C-3945
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US-09-562-737-125
US-09-248-796A-26397
US-09-543-681A-7295
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US-09-861-451A-16
US-09-438-185A-34
US-09-513-999C-4802
US-09-513-999C-4800
US-09-949-016-6012
US-09-949-016-11703
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S-09-438-185A-205
S-09-328-328-56400
S-09-270-767-41746
S-09-270-767-46116
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US-09-270-767-42959
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-09-540-236-2250
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Sequence 2055, Application US/09540236

Retent No. 6673910
GRNERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
SEQ ID NO 2859
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
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1 MSRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAOWQHKQTMLINEKKLNMMNA
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42.7%; Pred. No. 2.4e-17;
tive 15; Mismatches 35;
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27.0%; Score 131; DB 2;
Best Local Similarity 34.9%; Pred. No. 1.2e-08;
Matches 29; Conservative 13; Mismatches 41
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                                                                                                                                                  93 EDRKFLOOEMDKFLSGEDYAKADGYVP 119
                                                                                                  61 EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
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; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456
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Matches 38; Conservative
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US-09-540-236-2859
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US-09-540-236-2859
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                          0; Gaps
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                     Score 450; DB 2; Length 107;
Pred. No. 1.1e-48;
5; Mismatches 3; Indels
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Pred. No. 4.2e-41;
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80.0%; Pred. No. 4.2e-41;
ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                          61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
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                  92.6%;
91.2%;
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                  Query Match
Best Local Similarity 91.2
Matches 83; Conservative
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Matches 72; Conservative
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US-09-252-991A-23355
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US-09-543-681A-5443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5443
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Flint, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AWAQWQH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 KQTMLIN-----RKLLEQEMVNFLFEGK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                            30 IYNEISKEAWA-------QWQHKQTWLINEKKLNMMNAEHRKLLEQEMVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Anglogenesis Genes and Polypeptides
FILE REPERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
LENGTH: 1214
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08533669A
Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
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13.9%; Score 67.5; Di
Best Local Similarity 25.2%; Pred. No. 2.1;
Matches 34; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                             14.5%; Score 70.5; D
28.4%; Pred. No. 11;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 TFLOREAEGOD-FQLYPGELGKRIYNEISKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NOS: 206
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1004 IAEVKKOLELEKOOAVDETKK 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 LFEGK---EVHIEGYTPEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 EVDMHLASY--EAKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 EV--HIEGYTPEDKK 91
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.4
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-164-595-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-325-932A-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-325-932A-66
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SEQ ID NO 66
LENGTH: 184
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQ-WQH-KQTMLINEKKLNMMWNA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 RTLYQAMIITKSSKGDFLIRTKKDGKQIWEAASKTALKKSWKHYEQEMLKNEKVA---- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 BAEGODFOLYP-----GELGKRI-YNEISKBAWAQWQHKQTMLINEKKLINMMNAEHRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.6%; Score 76; DB 2; Length 548; Best Local Similarity 30.7%; Pred. No. 0.77; Matches 27; Conservative 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 72; DB 2; Length 474; 25.6%; Pred. No. 2; tive 18; Mismatches 28; Indels
                                                                      APPLICANT: Kron, Micheal
APPLICANT: Hartlein, Micheal
APPLICANT: Michito, Hirikata
TITLE OF INVENTION: Human Asparaginyl-tRNA Synthetase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRICH APPLICATION NUMBER: US 60/074,788
FRICH RILING DATE: 1998-02-18
FRICH RILING DATE: 1998-02-18
FRICH RILING DATE: 1998-07-27
SEQ ID NO 24473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --AKMLEKDATEVGVKAALEEAKKVQIE 103
                                                                                                                                                                  FILE REFERENCE: Aparaginyl-trna Synthetase
CURRENT APPLICATION NUMBER: US/09/167,299
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHRKLLEQEMVNF----LFEGKEVHIE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24473, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-164-595-24
; Sequence 24, Application US/10164595
; Patent No. 6657054
Sequence 3, Application US/09167299
Patent No. 6245539
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: P10723
DATABASE ENTRY DATE: 1997-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- MYDMLNKGETLPVD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 LEQEMVNFLFEGKEVHIE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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1 MSRIIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA 60
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APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.9%; Score 67.5; DE
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EHRKLLEQEMVNFLFEGKEVHIEG--YTPEDK
                                  FILING DATE: 12-FEB-1998
TTORNEY AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAIL.
COUNTY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"AWDITER: IBM PC compatible
"AWDITER: TO COMPATIBLE
"AWDITER: AWDITER: A
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Patent No. 6375955
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                         : 546 amino acids
amino acid
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-183-861-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-09-022-765-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-022-765-2
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA 60
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Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos Neto, Antonio
APPLICANT: Webb, John C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 546;
                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PPC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 222-4900
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EHRKLLEQEMVNFLFEGKEVHIEG--YTPEDK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 67.5; DI
; Pred. No. 8.9;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.3%;
Matches 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-533-669A-2
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
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STREET: 65.
CITY: Seattle
THE: Washington
                                                                                                                                               STATE: Washington
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                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-183-861-2
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33; Indels 21; Gaps
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APPLICATION NUMBER: 09/022,765
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John C.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
ITILE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
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3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue

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Query Match
Best Local Similarity 28.3%
Matches 26; Conservative
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Best Local Similarity
Matches 26; Conserva
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                                                                                                                                                                                                                                                                                                                      US-09-639-206A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-639-206A-2
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                                                                                                      301 MTRNALCLORORKYEAA-IDLY-----KRALVEWRNPDTL----KKLTECEK 342
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                                                                               1 MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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                                        21; Gaps
  Length 546;
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: TITLE OF INVENTION: THERMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
13.9%; Score 67.5; DB 2; Length 5
28.3%; Pred. No. 8.9;
tive 12; Mismatches 33; Indels
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                                                                                                                                                                                      ||:| :|: :: 343 EHQKAVEEAYIDPEI-AKQKKOEGNQYFKEDK 373
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                                                                                                                                                           EHRKILLEQEMVNFLFEGKEVHIEG--YTPEDK 90
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CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT FILING DATE: 2000-04-14
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Patent No. 6607731
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Campos-Neto, Antonio
Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
Peter Probst
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Best Local Similarity 28.3%
Matches 26; Conservative
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                                        Conservative
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                    Similarity
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SEQ ID NO 2
LENGTH: 546
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LENGTH: 546
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APPLICANT:
  Query Match
Best Local
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301 MTRNALCLORORKYBAA-IDLY-----KRALVBWRNPDTL----KKLTECEK 342
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                                                                                                    1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA 60
                                                   21; Gaps
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     DB 2; Length 546;
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                   33; Indels
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                                                                                                                                                                                                                                           143 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 EHQKAVEBAYIDPEI-AKQKKDEGNQYFKEDK 373
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13.9%; Score 67.5; DE
28.3%; Pred. No. 8.9;
ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Probst, Peter
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR
TITLE OF INVENTION: THERAPY AND DIAGNOSIS O
FILS REPERENCE: 210121.42007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/639,206A CURRENT FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09639206A Patent No. 6613337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09874923
Patent No. 6638517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto, Antonio
Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
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Skeiky, Yasir A.W.
Bhatia, Ajay
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ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
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JS-09-565-501A-95
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 95
LENGTH: 982
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                                                                                                                                                        Query Match 13.9%; Score 67.5; DB 2; Length 546; Best Local Similarity 28.3%; Pred. No. 8.9; Matches 26; Conservative 12; Mismatches 33; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08798841
Patent No. 6709661
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,841
                                                                                                                                                                                                                                                                                                                                             343 EHOKAVEEAYIDPEI-AKOKKDEGNOYFKEDK 373
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28.3%; Pred. No. o...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NIMBER: 210121.420C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 546
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CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.38
Matches 26; Conservative
                                                                            , TYPE: PRT
, ORGANISM: Leishmania major
US-09-874-923-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple OTHER INFORMATION: Leishmania antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSRIIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAOWQHKQTMLINEKKLNMMNA
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LICANT: Dillion, Davin C.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Bhatia, Ajay

APPLICANT: Coler, Rhea

APPLICANT: Peter Probet

ITILE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

ITILE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

FILE REFERENCE: 210121, 420.06

CURRENT APPLICATION NUMBER: US/09/565,501A

CURRENT FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 95

LENGTH: 982

IERGTH: 982
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                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, TASIR A.W.
APPLICANT: Skeiky, THERAPY AND DIAGNOSIS OF LEISHMANIASIS
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A
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Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches
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FastSEQ for Windows Version 4.0
Sequence 95, Application US/09551974A Patent No. 6500437 GENERAL INFORMATION:
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Best Local Similarity 28.33
Matches 26, Conservative
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SOPTWARE: FASTSEQ FOR
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2

21; Gaps

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1 MSRTIFCTFLQREAEGQDFQLYPGBLGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNA 60
                                                                      PEATURE:
OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
OTHER INFORMATION: Leishmania antigens
US-03-874-923-95
                                                                                                                                                                                          Query Match
13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 2:
LENGTH: 982
TYPE: PRT
ORGANISM: Artificial Sequence
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Bhatia, Ajay
Coler, Rhea
Peter Probst
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REPERENCE: 210121-420C7.
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
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TITLE OF INVENTION: LEESHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121,420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
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|51 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 581
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| EHQKAVEEAYIDPEI-AKQKXDEGNQYFKEDK 581
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 982
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
                                                                                                                                                                                                                                                              Sequence 95, Application US/09639206A
Patent No. 6613337
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
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Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
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Skeiky, Yasir A.W.
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Coler, Rhea
Probst, Peter
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APPLICANT: Reed, Steven G.

APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

FILE REFERENCE: 210.11.42065;

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14

SOFTWARE FESTES (for Windows V-

SEQ ID NO 97

LENGTH: 1427

TYPE: PPT
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551 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 581
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509 MTRNALCLORORKYBAA-IDLY----
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Campos-Neto, Antonio
Webb, John R.
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Search completed: June 27, 2007, 11:12:21 Job time : 52 secs
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USB IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS FILE REFERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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13.9%; Score 67.5; DB 2; Length 14:
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMAN FILE REFERENCE: 210121.420C7
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FASESO for Windows Version 4.0
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|551 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 581
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551 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 581
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13.9%; Score 67.5; I
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative, 12; Mismatches
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Webb, John R.
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ORGANISM: Artificial Sequence
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US-09-639-206A-97
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RESULT 25 US-09-874-923-97

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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.42008
CURRENT PLING DATE: 2001-06-04
CURRENT PLING DATE: 2001-06-04
SUMMER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
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|S51 EHQKAVEEAYIDPEI-AKQKKDEGNQYFKEDK 581
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Application US/09874923
                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
                                                                                                                                      Dillon, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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  Sequence 97,
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APPLICANT:
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Matches
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| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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Sequence 18,
Sequence 15,
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Sequence 20,
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Sequence 5,
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-09-955-502-26
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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	0		87	ო	-09-955-502-2	equence 29,
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	0	7	87	m	-09-955-502-3	equence 31,
	0		87	m	-09-955-502-3	equence 32,
			4	S	-10-450-763-4110	equence 4110
		Ġ	0	4	-10-282-122A-6813	equence 6813
		Ġ	4	4	-10-282-122A-6	equence 6602
	4.	'n	m	4	-10-369-493-1874	equence 1874
		2	œ	9	-11-087-099-202	equence 2028
	ä	4.	7	S	-10-805-684-10	equence 105,
	7	4	311	ß	-10-506-454-86	equence 86
		4	9	4	-10 - 416 - 330 - 3	equence 37,
		4	9	'n	-10-491-467-15	equence 15,
		4	œ	ß	-10-732-923-4	equence 4885
	ö	4	0	4	-10-085-198-144	equence 144,
	。	4	21	Ŋ	-10-717-665-2	equence 24,
	φ.	4	8	m	-09-934-455-46	equence 466,
	6	4.	8	4	-10-225-06	equence 180,
	6	4	8	4	-10-225-067-6	equence 64,
	φ.	4	æ	4	-10-374-780A-	equence 396,
	69.5	4	8	2	-10-225-066A-180	equence 180,
	6	4.	9	4	-10-437-963-1696	equence 169
	6	4	99	9	-11-097-143-24705	equence 247
	ď	4	9	4	-10-437-963-1891	equence 189
		4	S	4	-10-415-478A-36	equence 36,
	9	4	S	ß	-10-472-928-20	equence 206
		4.	œ	4	-10-393-840-52	equence 52,
57	-	14.0	102	٣	9-864-408A	76
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	67.5	m.	ω.	4	-10-393-840-118	equence 118
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		m .	4	· •	-09-991-496-2	equence 2,
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		·	N	~	-09-991-496-12	equence 178
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	۲.	÷	œ	m	-09-874-923-9	equence 95,
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	7	m	42	m	-09-874-923-9	equence 97,
	۲.	۳.	42	٣	-09-991-496-9	equence 97,
	7	ω.	4	m	-09-874-923-9	equence 96,
	7	۳.	64	m	-09-991-496-9	equence 96,
	67	ω.	8	9	-11-188-298-1626	equence 162
	9		6	9	-11-096-568A	equence 615
		m	N	9	-11-096-568A-615	equence 615
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## ALIGNMENTS

Sequence 11, Application US/0995502

Sequence 11, Application US/0995502

Sequence 11, Application US/0995502

Sequence 11, Application US/0995502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Grailick, Jeff M.

TITLE OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296, 97559

CURRENT APPLICATION NUMBER: 08/09/955,502

CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR APPLICATION NUMBER: 00-09-18

SOFTWARE: PATE: LONG-09-22

NUMBER OF SEQ ID NOS: 33

LENGTH: 91

LENGTH: 91

TYPE: PRT

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Best Local Similarity 100.
Matches 91; Conservative
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APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Lable Proteins
FILE REFERENCE: 960296.97559
CURRENT PAPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
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APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 06/234,588
PRIOR FILING DATE: 2000-09-22
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                                               Query Match
100.0%; Score 486; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.9e-47;
Matches 91; Conservative 0; Mismatches 0;
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Patent No. US20020072118A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 91
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SOFTWARE: PatentIn Ver. 3
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US-09-955-502-13
US-09-955-502-11
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DB 3; Length 91;

100.0%; Score 486;

Query Match

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Sequence 16, Application US/09955502
| Patent No. US20020072118A1 |
| GENERAL INPORMATION: |
| APPLICANT: Downs, Diana M. |
| APPLICANT: Gralnick, Jeff A. |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: UNMERS: US/09/955,502 |
| CURRENT APPLICATION NUMBER: US/09/955,502 |
| CURRENT PILING DATE: 2001-09-18 |
| PRIOR APPLICATION NUMBER: 60/234,588 |
| PRIOR FILING DATE: 2000-09-22 |
| NUMBER POLSE PATENTION OF SEQ ID NOS: 33 |
| SOFTWARE: PatentIn Ver. 2.1 |
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APPLICANT: Downs, Diana M.
APPLICANT: Drainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT PELLING NUMBER: US/09/955,502
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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Pred. No. 6.5e-45;
5; Mismatches 0; Indels
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                           Indels
100.0%; Pred. No. 7.9e-47; tive 0; Mismatches 0;
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                                                                                                                                                                                                                       BHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
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Patent No. US20020072118A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Salmonella paratyphi
US-09-955-502-14
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Best Local Similarity 94.5%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 96.5'
Best Local Similarity 94.5'
Matches 86; Conservative
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61 BHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                                                                        Sequence 15, Application US/09955502 Patent No. US20020072118A1
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Best Local Similarity 83.3%;
Matches 75; Conservative
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ORGANISM: Vibrio cholerae
US-09-955-502-10
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US-09-955-502-15
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Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97595
CURRENT FILING DATE: 2001-09-18
FRIOR APPLICATION NUMBER: 60/234,588
FRIOR APPLICATION NUMBER: 60/234,588
FRIOR APPLICATION NUMBER: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
LENGTH: 91
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                  1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINEKKLNMMNA 60
                                                                                                                                                                                                          Sequence 17, Application US/09955502

Fatent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION OXYGEN-Labile Proteins

FILE REFERENCE: 2001-09-18

CURRENT APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOSTWARE: PATENTIN Ver. 2.1
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MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNA
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Pred. No. 6.5e-45;
5; Mismatches 0; Indels
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Pred. No. 2.5e-43;
                                                                               91
                                                                                                    61 EHRKLLEQEMVSFLFEGKDVHIEGYTPEDKK 91
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; ORGANISM: Salmonella typhimurium
US-09-955-502-18
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Best Local Similarity 94.5%;
Matches 86; Conservative
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Best Local Similarity 92.3.
Best Local 84; Conservative
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LENGTH: 91
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Sequence 10, Application US/0995502;
Sequence 10, Application US/0995502;
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559;
CURRENT APPLICATION NUMBER: US/09/955,502;
CURRENT APPLICATION NUMBER: 60/234,588
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22;
NUMBER OF SEQ ID NOS: 33
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 10
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APPLICANT: Downs, Diana M.
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Myrgen-Labile Proteins
FILE REPERENCE: 960296-97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SSFTWARE: PALENTIN Ver. 2.1
SSGTU NO 15
LENGTH: 88
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Pred. No. 2.3e-37;
7; Mismatches 8; Indels
                         61 EHRKLLEQEMVSFLFEGKDVHIEGYPTEDKK 91
61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
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Sequence 5, Application US/0995502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: 0xygen-Labile Proteins

FILE REPRENCE: 960296.9759.

CURRENT APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.8%;
Best Local Similarity 76.9%;
Matches 70; Conservative 1:
                            -09-955-502-5
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                                                                                                              Sequence 20, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT PAPLICATION NUMBER: US/09/955,502
CURRENT PILING DATE: 2001-09-18
FRIOR PILING DATE: 2001-09-22
NUMBER OF SEQ ID NOS: 33
SOSTWARE: PatentIn Ver. 2.1
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Perent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Grainick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Method for Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR PILING DATE: 2000-09-22
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Pred. No. 1.1e-36;
8; Mismatches 8; Indels
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61 EHRKLLEQEMVNFLFEGKEVHIEGYTPPAK 90
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EHRKLLEQEMVQFLFEGK 78
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Best Local Similarity 82.2%;
Matches 74; Conservative
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Best Local Similarity 94.9<sup>†</sup>
Matches 74; Conservative
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SEQ ID NO 19
LENGTH: 78
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US-09-955-502-20
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                                                                          RESULT 10
US-09-955-502-20
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LENGTH: 90
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Gaps

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Length 91; Indels

; Score 388; DB 3; ; Pred. No. 8.7e-36; 11; Mismatches 10;

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                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
APPLICANT: Grainick, Jeff A.
APPLICANT: Grainick, Jeff A.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296 97559
CURRENT PELING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR PILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 7
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61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
                              EHRKLLEGEMVNFLFEGKDVHIEGYTPPEAK 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-955-502-6
; Sequence 6, Application US/09955502
                                                                                                                                                                                  Sequence 7, Application US/09955502 Patent No. US20020072118A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Haemophilus influenzae US-09-955-502-7
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Matches 68; Conservative
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RESULT 17
US-09-955-502-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Method for Proteins
FILE REPERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT APPLICATION NUMBER: 60/234,588
PRIOR RILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                    APPLICANT: Downs, Diana M.
APPLICANT: Downs, Diana M.
APPLICANT: Oralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells of TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960.296.975.59
CURRENT APPLICATION UNMERR: 00/955,502
CURRENT PILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Patent No. US20020072118A1
GENERAL INFORMATION:
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Patent No. US20020072118A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-955-502-6
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Matches 66; Conservative
NO. US20020072118A1
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US-09-955-502-9
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LENGTH: 87
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APPLICANT: Downs, Diana M

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TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Method for Proteins TITLE OF INVENTION: Oxygen-Labile Proteins FILE REPERENCE: 960296.97559
CURRENT APPLICATION NUMBER: U5/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 88
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| Sequence 21, Application US/09955502
| Patent No. US20020072118A1
| SAPPLICANT: Downs, Diana M. |
| APPLICANT: Downs, Diana M. |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| FILE REFERENCE: 960296.97539
| CURRENT APPLICATION NUMBER: 00/09-18 |
| PRIOR APPLICATION NUMBER: 00/234,588 |
| PRIOR FILING DATE: 2000-09-22 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 21 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Downs, Diana M. PapLICANT: Grahhick, Jeff A. TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Oxygen-Labile Proteins
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68.2%; Pred. No. 1.7e-29;
tive 12; Mismatches 16
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Patent No. US20020072118A1
GENERAL INFORMATION:
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61 EHRKKIEKYMKLFLFK 76
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Best Local Similarity 68.2%
Matches 60; Conservative
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US-09-955-502-21
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1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA 60
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Eatent No. US2022072116A1
GENERAL INFORMATION:
APPLICANT: Downs, Diama M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
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Patent No. US20020072118A1
Patent No. US20020072118A1
Patent No. US20020072118A1
Patent No. US20020072118A1
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
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8.1e-21;
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Pred. No. 8.1e-21;
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FILE REFERENCE: 960296.97559
CURRENT PAPPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR PLING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.1
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PRIOR FILING DATE: 2000-09-22
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US-09-955-502-3
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; ORGANISM: Bordetella pertussis
US-09-955-502-2
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SEQ TON 0 3
LENGTH: 87
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Best Local Similarity
Matches 48; Conserve
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Best Local Similarity
Matches 48; Conserv
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US-09-955-502-4
                                                                                                                                                               SEQ ID NO 2
LENGTH: 87
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1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIWQQISKEAWEEWKQIQTRLVNENRLNLADA 60
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APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR PILING DATE: 2000-09-22
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APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNA
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49.6%; Score 241; DB 3; Length 86;
Best Local Similarity 54.8%; Pred. No. 3e-19;
Matches 46; Conservative 13; Mismatches 25; Indels
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PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 86
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PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                      ; ORGANISM: Bordetella bronchiseptica
US-09-955-502-4
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Patent No. US20020072118A1
GENERAL INFORMATION:
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US-09-955-502-25
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 87
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                                                                                                                                                                   TYPE: PRT
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US-09-955-502-24
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Sequence 22, Application US/0995502;
Batent No. US2002007118A1;
GENERAL INCRMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Method for Proteins
TITLE OF INVENTION: UNSUREN: US/09/955,502
CURRENT APPLICATION NUMBER: US/09/955,502;
CURRENT APPLICATION NUMBER: 60/234,588
PRIOR PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                 Sequence 23, Application US/0995502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REPERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT PILING DATE: 2001-09-18
PRIOR PILING DATE: 2000-09-22
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                                                                                                                                      ch 46.7%; Score 227; DB 3; Length 88; L Similarity 50.0%; Pred. No. 1.2e-17; 44; Conservative 16; Mismatches 28; Indels
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47.8%; Pred. No. 1.2e-17;
tive 15; Mismatches 32; Indels
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61 KARQFLEQEMINFLFGTGSEKPAGYTSE 88
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                                                            ; TYPE: PRT
; ORGANISM: Coxiella burnetii
US-09-955-502-33
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 88
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SEQ ID NO 22
LENGTH: 89
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SOFTWARE: Patentin Ver.;
                                                                                                                                          Query Match
Best Local Similarity
Matches 44; Conserv
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Best Local Similarity
Matches 43; Conserv
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LENGTH: 90
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Sequence 24. Application US/09955502

Patent NO. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Oxygen-Labile Proteins
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REPERENCE: 960296 97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                             1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTWLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNNA
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                                                                                                                                               34; Indels
                                                                                            ch 46.5%; Score 226; DB 3;
1. Similarity 50.6%; Pred. No. 1.5e-17;
45; Conservative 10; Mismatches 34.
                                                                                                                                                                                                                                                                                                 61 EHRKLLEQEMVNPLFEGKEVHIEGYTPED 89
                                                                                                                                                                                                                                                                                                                                61 EHRKLLEQEMVNFLFEGKE-VHIEGYTP 87
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ORGANISM: Pseudomonas putida
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-09-955-502-22
                                                                                                 Query Match
Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                       June 27, 2007, 11:26:12; Search time 141 Seconds (without alignments) 221.752 Million cell updates/sec
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1: /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /EWC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRTIFCTFLQREAEGQDFQ......NFLFEGKEVHIEGYTPEDKK
                                                     GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-419-128-23355
US-11-603-108-2859
US-11-516-230-44283
US-11-516-230-44283
US-11-516-230-44293
US-11-516-230-44263
US-11-516-230-44271
US-10-526-324-706
US-10-526-324-706
US-10-516-230-44261
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US-11-443-428A-890383
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US-11-582-861-6675
US-11-443-428A-890395
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Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 890402, Sequence 890378, Sequence 890382, Sequence 890381, Sequence 890391, Sequence 890391, Sequence 890391, Sequence 890391, Sequence 6714, App Sequence 6713, App Sequence 81002, Sequence 810112, Sequence 81010, Sequence 81010, Sequence 81010, Sequence 81011, App Sequence 81011, App Sequence 81181, App Sequence 919550, Sequence 9171, App Sequence 2171, A	SEQUENCES RELATING TO PSEUDOMONAS AND THERAPEUTICS
1135 7 US-11-443-428A-890402 1135 7 US-11-443-428A-8903392 1140 7 US-11-443-428A-8903392 1140 7 US-11-443-428A-8903392 1142 7 US-11-443-428A-8903393 1143 7 US-11-443-428A-8903393 1159 7 US-11-443-428A-8903393 1160 7 US-11-443-428A-8903393 1186 7 US-11-443-428A-8903393 1186 7 US-11-443-428A-8903393 1186 7 US-11-443-428A-8903393 1186 7 US-11-582-861-6673 1186 7 US-11-582-861-6673 1186 7 US-11-582-861-0673 1186 7 US-11-443-428A-861008 1186 7 US-11-582-861-0673 1186 7 US-11-443-428A-861009 1186 7 US-11-443-428A-861009 1187 0 US-11-443-428A-861009 1188 7 US-11-443-428A-861009 1189 7 US-11-443-428A-861009 1189 7 US-11-443-428A-861009 1189 7 US-11-443-428A-861009 1180 7 US-11-443-428A-861009 1181 7 US-11-486-448-655050 1181 7 US-11-330-403-983 1181 7 US-11-330-403-983 1181 7 US-11-330-403-984 1181 7 US-11-330-403-984	ALIGNMENTS on US/10419128 10624A1 field et al. ELC ACID AND AMINO ACID SEQUEN UGINOSA FOR DIAGNOSTICS AND TH 36 318 318 31003-04-21 3105/09/252,991 3105/09/252,991 3105/09/252,991 3105/09/252,991 3105/09/252,991 3105/09/252,991
26 70.5 14.5 1113 2	RESULT 1  US-10-419-128-23355  Sequence 23355, Application US/10419128  Publication No. US20070020624A1  GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE; CURRENT ELER REFERENCE: 107196.136  CURRENT APPLICATION NUMBER: US/09/252,991  PRIOR PRILING DATE: 1999-02-18  PRIOR PILING DATE: 1999-02-18  PRIOR FILING DATE: 1999-02-18

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Gaps
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PRIOR FILING DATE: 2006-02-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Blomax PatentTool according to PatentIN 3.1 format
SEQ ID NO 44315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Looser, Ralf
TILE OF INVENTION: Process for the production of fine chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 DFQLYPGELGKRIY-NEISKEAWAQWQHKQTMLINEKKLNMMNAEHRKL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%; Score 85.5; 38.8%; Pred. No. 2.
                                                                                                                            PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110418.8
PRIOR PILING DATE: 2006-02-24
PRIOR PILING DATE: 2006-02-24
PRIOR FILING DATE: 2006-02-24
PRIOR FILING DATE: 2006-02-24
PRIOR PADELICATION NUMBER: EP 06110378.4
PRIOR APPLICATION NUMBER: EP 06110378.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Desulfotalea psychrophila LSv54
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                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110327.1
PRIOR FILING DATE: 2006-02-23
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APPLICATION UNUBER: EP 06110579.7
FILING DATE: 2006-02-28
APPLICATION NUMBER: EP 06110425.3
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PAPLICATION NUMBER: EP 06110423.8
APPLICATION NUMBER: EP 06110418.8
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APPLICATION NUMBER: EP 06110383.4
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APPLICATION NUMBER: EP 06110378.4
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Publication No. US20070118916A1
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Schauwecker, Florian
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Matches 19; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FITLE PEPERENCE: PATHO3-14
CURRENT PRINCE PATHO3-14
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 69/540,263
PRIOR FILING DATE: 2000-04-04
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2859
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APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTIONS: Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR FILING DATE: 2006-02-24
                                                                                                                                                       Query Match 47.5%; Score 211; DB 6; Length 122; Best Local Similarity 51.7%; Pred. No. 3.4e-16; Matches 45; Conservative 10; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.0%; Score 131; DB 6; Length 110; 34.9%; Pred. No. 7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         93 EDRKFLQQEMDKFLSGEDYAKADGYVP 119
                                                                                                                                                                                                                                                                                                                                                                        61 EHRKLLEQEMVNFLFEGKEVHIEGYTP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44315, Application US/11516230 Publication No. US20070118916A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2859, Application US/10603108; Publication No. US20070010665A1; GENERAL INFORMATION:
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                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-419-128-23355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herold, Manfred
Wendel, Birgit
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APPLICANT: Puzio, Piotr
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US-10-603-108-2859
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Best Local Similarity
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US-11-516-230-44315
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SEQ ID NO 23355
LENGTH: 122
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                      Gaps
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
SEQ ID NO 44283
LENGTH: 507

    See File Wrapper or PALM.

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APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTION Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
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SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
                                                                                                                                                                                                                                                                        Query Match 16.7%; Score 81; DB 7; Length 507; Best Local Similarity 28.2%; Pred. No. 6.3; Matches 22; Conservative 16; Mismatches 28; Indels
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ORGANISM: Chromobacterium violaceum ATCC 12472
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PRIOR PELING DATE: 2006-05-05
PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR APPLICATION NUMBER: EP 06110425.3
PRIOR PILING DATE: 2006-02-28
PRIOR PELING DATE: 2006-02-24
PRIOR PELING DATE: 2006-02-24
PRIOR PELING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110418.8
PRIOR PILING DATE: 2006-02-24
PRIOR PILING DATE: 2006-02-24
PRIOR PILING DATE: 2006-02-24
PRIOR PILING DATE: 2006-02-24
PRIOR PLING DATE: 2006-02-24
PRIOR PELING DATE: 2006-02-24
PRIOR PELING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110378.4
PRIOR PELING DATE: 2006-02-24
PRIOR PELING DATE: 2006-02-23
PRIOR PELING DATE: 2006-02-23
PRIOR PELING DATE: 2006-02-23
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Publication No. US20070118916A1
GENERAL INFORMATION:
                                                                                                                                                     TYPE: PRT ORGANISM: Pseudomonas putida KT2440
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                                                                                                                                                                                                                   US-11-516-230-44283
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US-11-516-230-44299
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LENGTH: 508
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311 YDASSGKRVDLDKITKEEVASWQPGDVLLLANGKILTGRDAAHKR-----MIDMLNKGEKL 365
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APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Rall
TITLE OF INVENTION: Process for the production of fine chemicals
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PRIOR FILING DATE: 2006-02-28

PRIOR FILING DATE: 2006-02-28

PRIOR FILING DATE: 2006-02-24

PRIOR PILING DATE: 2006-02-24

PRIOR PILING DATE: 2006-02-24

PRIOR PLILING DATE: 2006-02-24

PRIOR APPLICATION NUMBER: EP 06110418.8

PRIOR FILING DATE: 2006-02-24

PRIOR APPLICATION NUMBER: EP 06110383.4

PRIOR APPLICATION NUMBER: EP 06110383.4

PRIOR APPLICATION NUMBER: EP 06110387.4

PRIOR APPLICATION NUMBER: EP 06110387.7

PRIOR PILING DATE: 2006-02-24

PRIOR PILING DATE: 2006-02-24

PRIOR PLING DATE: 2006-02-24

PRIOR PLING DATE: 2006-02-23

PRIOR PLING DATE: 2006-02-33

PRIOR PLING DATE: 2006-02-33
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CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
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PRIOR FILING DATE: 2006-09-06
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US-11-516-230-44263
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Best Local Similarity 30.2%
Matches 19; Conservative
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Gaps

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Query Match 15.5%; Score 75.5; Di
Best Local Similarity 27.3%; Pred. No. 24;
Matches 21; Conscrvative 15; Migmatches
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LOCATION: (786890)..(786890)
OTHER INFORMATION: n is a or c or g or t.
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Ralstonia solanacearum GMI1000
                                                                                                                APPLICATION NUMBER: EP 06110383.4
FILING DATE: 2006-02-24
APPLICATION NUMBER: EP 06110378.4
                                       PLICATION NUMBER: EP 06110423.8
                                                          FILING DATE: 2006-02-24
APPLICATION NUMBER: EP 06110418.8
06110425.3
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Publication No. US20060248617A1
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                                                                                                 FILING DATE: 2006-02-24
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OTHER INFORMATION: n is a or
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LOCATION: (786907)..(786907)
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LOCATION: (4145
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                                                                                               APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fine chemicals
TILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Blomax PatentTool according to PatentIN 3.1 format SEQ ID NO 44265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.0%; Score 78; DB 7; Length 546; 30.2%; Pred. No. 14; tive 18; Mismatches 20; Indels
                                                                                                                                                                                          APPLICANT: LOOSEr, Ralf
TITLE OF INVENTION: Process for the produc
FILE REFERENCE: 13195-0014-US
CURENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 73449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR FILING DATE: 2006-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44271, Application US/11516230 Publication No. US20070118916A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schauwecker, Florian
Looser, Ralf
                                                                              Schauwecker, Florian
Looser, Ralf
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Herold, Manfred
Wendel, Birgit
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Best Local Similarity 30.2%
Matches 19; Conservative
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                                                              Kamlage, Beate
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405 PVD 407
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APPLICANT: Imanaka, Takayuki
APPLICANT: Imanaka, Takayuki
APPLICANT: Imanaka, Takayuki
APPLICANT: Imanaka, Takayuki
TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME CHIP USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 490051.401USPC
CURRENT APPLICATION NUMBER: US/10/526,324
CURRENT PILING DATE: 2005-02-28
PRIOR FILING DATE: 2003-08-29
PRIOR PLICATION NUMBER: DF2/182003/003597
PRIOR APPLICATION NUMBER: DF2/182003/003597
PRIOR PLILING DATE: 2003-08-30
NUMBER OF SEQ ID NOS: 2167
SOFTWARE: Patentin version 3.1
SEQ ID NO 706
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 EGQDFQLYP-----GELGKRI-YNEISKEAWAOWOHKOTWLINEKKLNWMNAEHRKLL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels 13; Gaps
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110367.7
PRIOR PILING DATE: 2006-02-24
PRIOR FILING DATE: 2006-02-23
PRIOR PILING DATE: 2006-02-23
PRIOR APPLICATION NUMBER: EP 06110325.5
PRIOR FILING DATE: 2006-02-23
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax Patentrool according to PatentIN 3.1 format SEQ ID NO 4271
LENGTH: 507
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299 ELEAPSLDAYPEIVWEAGPSARRVDLDKITPEEVQSWKPGETLLLNGKMLTGRDAAHKR- 357
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PRIOR FILING DATE: 2006-02-24
PRIOR PILING DATE: 2006-02-24
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110327.1
PRIOR APPLICATION NUMBER: EP 06110325.5
PRIOR PILING DATE: 2006-02-23
PRIOR FILING DATE: 2006-02-23
PRIOR FILING DATE: 2006-02-23
PRIOR FILING DATE: 2006-02-23
PRIOR PILING DATE: 2006-02-23
PRIOR FILING DATE: 2006-02-23
PRIOR FILING DATE: 2006-02-23
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APPLICANT: Schauwecker, Florian
APPLICANT: Losser, Rall
TITLE OF INVENTION: Process for the production of fine chemicals
                                                                                                                                                                                                                                                                            ; DB 6; Length 474;
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SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
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54;
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CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
                                                                                                                                                                                                                                                                            14.8%; Score 72; 25.6%; Pred. No.
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DAFE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 24473
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PRIOR PAPLICATION NUMBER: EP 06110579.7
PRIOR PILING DATE: 2006-02-28
PRIOR APPLICATION NUMBER: EP 06110425.3
PRIOR PILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110423.8
PRIOR PILING DATE: 2006-02-24
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US-11-516-230-44261
; Sequence 44261, Application US/11516230
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                                                                                                                                                                                                     , ORGANISM: Pseudomonas aeruginosa
US-10-419-128-24473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LEQEMVNFLFEGKEVHIE 83
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Best Local Similarity 25.65
Matches 20; Conservative
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APPLICANT: Puzio, Piotr
APPLICANT: Blau, Astrid
APPLICANT: Herold, Manfred
APPLICANT: Wendel, Birgit
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Best Local Similarity 25.6
Matches 20; Conservative
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Publication No. US20070020624A1
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 EGODFQLYPGE-----KKLINMMNA 60
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; Pred. No. 15;
13; Mismatches 29; Indels
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OCATION: (1128517)..(1128518)
WHER INFORMATION: n is a or c or g or t.
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OCATION: (1128539)..(1128540)
VTHER INFORMATION: n is a or c or g.or t.
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LOCATION: (1561477)..(1561477)
DTHER INFORMATION: n is a or c or g or t.
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LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a or c or g or t.
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LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a or c or g or t.
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CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
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                                                                                                                                                  NAME/KEY: misc feature
OCATION: (839139)..(839139)
OTHER INFORMATION: n is a or c or g
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ION: (1128488)..(1128488)
INFORMATION: n is a or c or g
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COCATION: (1128499)..(1128499)
DTHER INFORMATION: n is a or c or g
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COCATION: (1128505)..(1128506)
DTHER INFORMATION: n is a or c or g
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INFORMATION: n is a or c or
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                                                   AME/KEY: misc feature
ACATION: (786544)..(786946)
THER INFORMATION: n is a or c
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Best Local Similarity
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8

g 8

21; Gaps

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LOCATION: (304)...(352)
OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
OTHER INFORMATION: accession number BL00226B, p-value=6.337e-09, raw score of 23.86
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APPLICANT: SHII, SHIZUKO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: WAKAMATSU, AI
APPLICANT: MACAI, KEIICHI
APPLICANT: NGGAI, FERICHI
APPLICANT: PINSUI
FILE REFERENCE: 084335/0123
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: DOMAIN
LOCATION: (400)...(436)
OTHER INFORMATION: MYND finger domain identified by PFam, accession name OTHER INFORMATION: MYND, E-value=0.0097, PFam score of 10.4
                                                                                                                                                                                                                                                                                                                                                                              ----AQWQHKQTMLINEKKLNMMNAEHRKLLEQEMV 71
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                                                                                                                                                                                                                                                                     DB 6; Length 566;
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                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                     Query Match
14.7%; Score 71.5; DE
Best Local Similarity 28.9%; Pred. No. 70;
Matches 24; Conservative 10; Mismatches
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28.4%; Pred. No. 40;
tive 10; Mismatches
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PRIOR PLING DATE: 1999-07-29
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-09
PRIOR PELING DATE: 2000-05-09
PRIOR PELING DATE: 2000-05-09
PRIOR PLING DATE: 1999-10-18
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PRIOR APPLICATION NUMBER: JP 1999-248036
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PRIOR FILING DATE: 2000-07-28
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Publication No. US20070105122A1
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PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                 30 IYNEISKE-AW-----
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APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
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Best Local Similarity 28.49
Matches 23; Conservative
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US-10-917-503-11063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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APPLICANT: Rotalic, David K.
APPLICANT: Andersen, Scott E.
APPLICANT: Andersen, Scott E.
APPLICANT: Connec, Timothy W.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Associated With
ITILE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
ITILE OF INVENTION: Plants
ITILE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
ITILE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
ITILE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
ITILE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
ITILE OF INVENTION: Number: US/10/703,032
CURRENT APPLICATION NUMBER: 10/20,338
PRIOR PELING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 211164
SEQ ID NO 118890
                                                                  13 EAEGODFOLYP-----GELGKRI-YNEISKEAWAQWQHKQTMLINEKKLNNMNAEHRKL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 FLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAEHRKLLEQ 68
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; APPLICANT: Hyseq, Inc.; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES; FILE REFERENCE: 21272-104; CURRENT APPLICATION NUMBER: US/10/276,817B; CURRENT FILING DATE: 2002-11-18; PRIOR FILING DATE: 2001-05-16; PRIOR FILING DATE: 2001-05-16; PRIOR FILING DATE: 2001-05-18; NUMBER OF SEQ ID NOS: 16102; SOFFWARE: CLECOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_TA_13308.pep
US-10-703-032-118890
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14.7%; Score 71.5; D
Best Local Similarity 25.6%; Pred. No. 11;
Matches 20; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                          ; Sequence 118890, Application US/10703032; Publication No. US20070044171A1; GENERAL INFORMATION:
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                                                                                                                                                                          ----MVDMLNKGETLPVD 366
                                                                                                                                       66 LEQEMVNFLFEGKEVHIE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 ENLDFMDCILEEGDMLYI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-276-817B-12931
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LENGTH: 566
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PPLICANT: Bernstein, Jeanne
ITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
                                                                                                                                                           --- QWQHKQTMLINEKKLINMMNAEHRKLLEQEMVNF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- OWOHKOTMLINEKKLINMMNAEHRKLLEQEMVNF 73
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Jackson, Donald
APPLICANT: Wong, Tai W.
TITLE OP INVENTION BIOWARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PCT
                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 614;
                                                       DB 7; Length 313;
                                                                                                Indels
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                                                                                                29;
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                                                       ; Score 70.5; D
; Pred. No. 44;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
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Pred. No. 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/567,867
CURRENT FILING DATE: 2006-01-27
PRIOR APPLICATION NUMBER: US 60/490,890
PRIOR PILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 2786
SOFTWARE: Patentin version 3.2
SEQ ID NO 1402
LENGTH: 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 890383, Application US/11443428A Publication No. US20070083334A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       US-10-567-867-1402
; Sequence 1402, Application US/10567867
; Publication No. US20070105114A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                         103 IAEVKKOLELEKOOAVDETKK 123
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                                                                                                                                                                                                                     74 LFEGK---EVHIEGYTPEDKK 91
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                                                           14.5%;
28.4%;
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Freilich, Shiri
Beck, Nili
Zhu, Wei-Yong
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Best Local Similarity 28.4%
Matches 23; Conservative
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Hermesh, Chen
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                                                                                                23; Conservative
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APPLICANT: Xie, Hanging
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US-10-567-867-1402
; ORGANISM: Homo sapiens
US-11-443-428A-890388
                                                         Query Match
Best Local Similarity
Matches 23; Conserv
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
TITLE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,428A
CURRENT PILING DATE: 2006-05-31
NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: Patentin version 3:1
LENGTH: 313
TYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL, FOR ANNOTATING BIOMOLECULAR SEQUENCES
43 IYNDLSKNTTGSTIABIRRLRIBIEKLQWLHQQELSEMKHNLELTMAEMRQSLEQERDRL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QWQHKQTMLINEKKLNMMNAEHRKLLEQEMVNF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 313;
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10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/443,428A CURRENT FILING DATE: 2006-05-31
                                                                                                                                                                          Sequence 890387, Application US/11443428A Publication No. US20070083334A1 GENERAL INFORMATION:
APPLICANT: Mintz, Liat APPLICANT: Xie, Hanqing APPLICANT: Dahari, Dvir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 890388, Application US/11443428A Publication No. US20070083334A1 GENERAL INFORMATION:
APPLICANT: Mintz, Liat APPLICANT: Xie, Hanging
                                                                             103 IAEVKKOLELEKOOAVDETKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 IAEVKKOLÉLEKOGAVDETKK 123
                                      74 LFEGK---EVHIEGYTPEDKK 91
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Hermesh, Chen
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Freilich. Shiri
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Zhu, Wei-Yong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-443-428A-890387
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Best Local Similarity
Matches 23; Conserv
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30 IYNEISKEAWA----
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APPLICANT: Mintz, Liat
APPLICANT: Xie, Hanging
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                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-11-582-861-6676
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US-11-582-861-6675
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APPLICANT:
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                                                                                                                                                                                                                                                         ----QWQHKQTMLINEKKINMMNAEHRKLLEQEMVNF 73
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                                                                                                                                                                                               Gaps
                                                                                                                                                      14.5%; Score 70.5; DB 7; Length 647; 28.4%; Pred. No. 1e+02; rative 10; Mismatches 29; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 702;
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APPLICANT: Zhang, Hui
APPLICANT: Zhang, Hui
APPLICANT: Aebersold, Rudolf H.
TITLE OF INVENTION: TISSUB- AND SERUM-DERIVED GLYCOPROTEINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: 4660092.404
CURRENT APPLICATION NUMBER: US/11/582,861
CURRENT FILING DATE: 2006-10-17
PRIOR APPLICATION NUMBER: US 60/728,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 70.5; DB 6;
; Pred. No. 1.1e+02;
10; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: FS606F1
CURRENT PELLOATION NUMBER: US/10/405,027
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/369,608
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR SPLICATION NUMBER: 60/376,175
PRIOR SPELICATION NUMBER: 50.00
NUMBER OF SEQ ID NOS: 5810
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (4)
COTHER INFORMATION: Xaa equals any amino acid
US-10-405-027-3329
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3329, Application US/10405027
Publication No. US20070015271A1
GENERAL INFORMATION:
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Sequence 6676, Application US/11582861
Publication No. US20070099251A1
GENERAL INFORMATION:
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28.4%;
NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: PatentIn version 3.1
SEQ ID NO 890383
                                                                                                                                      Query Match
Best Local Similarity 28...
Best Local Similarity 28...
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Best Local Similarity 28.49
Matches 23, Conservative
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                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890383
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US-10-405-027-3329
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LENGTH: 702
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522 IYNDLSKNTTGSTIAEIRRLRIEIEKLÖWLHQÖELSEMKHNLELTMÄEMRQSLEQERDRL 581
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                                                                                                                                                                                                                                                                                    Indels 19;
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; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
APPLICANT: Abelesold, Rudolf H.
; TITLE OF INVENTION: AID METHODS OF THEIR USE
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT PILING DATE: 2006-10-17
; PRIOR PILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 6675
; LENGTH: 995
                                                                                                                                                                                                                              Query Match
14.5%; Score 70.5; DB 7; Length 764;
Best Local Similarity 28.4%; Pred. No. 1.38+02;
Matches 23; Conservative 10; Mismatches 29; Indels 15
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14.5%; Score 70.5; DB 7;
Best Local Similarity 28.4%; Pred. No. 1.7e+02;
Matches 23; Conservative 10; Mismatches 29;
PRIOR FILING DATE: 2005-10-17
NUMBER OF SEQ ID NOS: 14918
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6676
LENGTH: 764
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Bernstein, Jeanne
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Wasserman, Alon
Hermesh, Chen
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Levanon, Brez
Freilich, Shiri
Beck, Nili
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APPLICANT: Azar, Idit
APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,428A
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEPUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/21929
CURRENT APPLICATION NUMBER: US/11/443,428A
CURRENT FILING DATE: 2006-05-31
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; Sequence 890396, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 890399
LINGTH: 1107
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SOFTWARE: Patentin version 3.1
SEQ ID NO 890396
LENGTH: 1115
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Wasserman, Alon
Hermesh, Chen
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Zhu, Wei-Yong
Wasserman, Alon
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APPLICANT: Xie, Hanging
APPLICANT: Dahari, Dvir
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US-11-443-428A-890399
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US-11-443-428A-890396
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TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/23929
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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830 IYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKHNLELTWAEMRQSLEQERDRL 889
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830 IYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKHNLELIWAEMRQSLEQERDRL 889
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14.5%; Score 70.5; DB 7;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29;
              FILE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,426A
CURRENT FILING DATE: 2006-05-31
NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: Patentin version 3.1
SEQ ID NO 890379
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Best Local Similarity 28...
Best Local 3, Conservative
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Freilich, Shiri
Beck, Nili
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Hermesh, Chen
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APPLICANT: Xie, Hanging
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US-11-443-428A-890395
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US-11-443-428A-890379
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